



SEQUENCE LISTING

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O'Connell, Ann P.

<120> Fruit Flavour Related Genes And Use Thereof

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<140> US/09/857,518
<141> 2002-03-29

<150> EP 98204018.0
<151> 1998-12-02

<150> EP 99200739.3
<151> 1999-03-12

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<170> PatentIn Ver. 2.1

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Tyr Ser Ser Val Gly Tyr Ser Leu Leu Lys Lys Glu Lys Ala Ile			
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att gtg cag cca gat cgt gtg acg ata ggg aat ggc cct aca ttt ggt			1166
Ile Val Gln Pro Asp Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly			
350	355	360	
tgt gtt ctc atg aag gat ttc ctc tta ggc cta gca aag aag ctg aag			1214
Cys Val Leu Met Lys Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys			
365	370	375	
cat aac aac act gct cat gag aac tac cgc agg atc ttt gtg cct gat			1262
His Asn Asn Thr Ala His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp			
380	385	390	395
ggc cac cct ctg aag gct gca ccc aaa gaa cct ttg agg gtt aat gtt			1310
Gly His Pro Leu Lys Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val			
400	405	410	
ctg ttc aaa cac att cag aat atg ctg tca gct gaa acc gct gtg att			1358
Leu Phe Lys His Ile Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile			
415	420	425	
gct gag aca ggg gac tca tgg ttt aac tgt cag aag ctg aaa ttg cca			1406
Ala Glu Thr Gly Asp Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro			

430	435	440	
ccc ggc tgc ggg tat gag ttc caa atg caa tat gga tca att ggt tgg Pro Gly Cys Gly Tyr Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp 445	450	455	1454
tca gtt gga gca act ctt ggg tat gct cag gct gta cct gag aag cga Ser Val Gly Ala Thr Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg 460	465	470	1502
gtg att tct ttc att ggt gat ggg agc ttc cag gtg act gct caa gat Val Ile Ser Phe Ile Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp 480	485	490	1550
gtg tcc aca atg att cga aat gga cag aga acc att att ttc ctg ata Val Ser Thr Met Ile Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile 495	500	505	1598
aac aat ggt gga tac acc att gaa gtg gaa atc cat gat gga cca tac Asn Asn Gly Gly Tyr Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr 510	515	520	1646
aat gtg atc aag aac tgg aac tac act gga ctg gtt gat gca atc cac Asn Val Ile Lys Asn Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His 525	530	535	1694
aat ggg gaa ggc aag tgc tgg aca acc aag gtg cgt tgc gaa gag gag Asn Gly Glu Gly Lys Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu 540	545	550	1742
ctg att gaa gca ata gag act gca aat gga ccc aag aag gat agc ttc Leu Ile Glu Ala Ile Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe 560	565	570	1790
tgc ttc att gag gtg att gtt cac aag gat gat acc agc aaa gag ttg Cys Phe Ile Glu Val Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu 575	580	585	1838
ctt gag tgg ggg tct agg gtt tct gct gcc aac agc cgc cca cct aat Leu Glu Trp Gly Ser Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn 590	595	600	1886
cct cag taaaactctc ctgtgtcata tgaaggcctt cattcacatt cacagattta Pro Gln 605			1942
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Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp Ala
5 10 15

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Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg Arg
20 25 30

gaa acc gga gag aaa gac gtg acg ttc aaa gtg atg tac tgt ggg att 202
Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly Ile
35 40 45

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Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr
50 55 60 65

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Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val
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Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly
85 90 95

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Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu
100 105 110

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Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly																																																																																													
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<210> 6																																																																																													
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<220>

<223> Strawberry alcohol acyl transferase

<400> 6

Met Glu Lys Ile Glu Val Ser Ile Asn Ser Lys His Thr Ile Lys Pro
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Ser Thr Ser Ser Thr Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
20 25 30

Gln Leu Thr Pro Pro Ala Tyr Val Pro Ile Val Phe Phe Tyr Pro Ile
35 40 45

Thr Asp His Asp Phe Asn Leu Pro Gln Thr Leu Ala Asp Leu Arg Gln
50 55 60

Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
65 70 75 80

Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
85 90 95

Glu Ala Arg Val Asn Cys Asp Met Thr Asp Phe Leu Arg Leu Arg Lys
100 105 110

Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
115 120 125

Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Val
130 135 140

Phe Asp Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
145 150 155 160

Asp Gly Gly Thr Ala Asp Cys Phe Leu Lys Ser Trp Gly Ala Val Phe
165 170 175

Arg Gly Cys Arg Glu Asn Ile Ile His Pro Ser Leu Ser Glu Ala Ala
180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Val Asp Gln
195 200 205

Met Glu Ala Leu Trp Phe Ala Gly Lys Lys Val Ala Thr Arg Arg Phe
210 215 220

Val Phe Gly Val Lys Ala Ile Ser Ser Ile Gln Asp Glu Ala Lys Ser
225 230 235 240

Glu Ser Val Pro Lys Pro Ser Arg Val His Ala Val Thr Gly Phe Leu
245 250 255

Trp Lys His Leu Ile Ala Ala Ser Arg Ala Leu Thr Ser Gly Thr Thr
260 265 270

Ser Thr Arg Leu Ser Ile Ala Ala Gln Ala Val Asn Leu Arg Thr Arg
275 280 285

Met Asn Met Glu Thr Val Leu Asp Asn Ala Thr Gly Asn Leu Phe Trp
 290 295 300
 Trp Ala Gln Ala Ile Leu Glu Leu Ser His Thr Thr Pro Glu Ile Ser
 305 310 315 320
 Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
 325 330 335
 Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Lys Gly Lys Glu Gly Tyr
 340 345 350
 Gly Arg Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
 355 360 365
 Glu Pro Ala Pro Asp Ile Tyr Leu Phe Ser Ser Trp Thr Asn Phe Phe
 370 375 380
 Asn Pro Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
 385 390 395 400
 Gly Lys Ile Glu Ser Ala Ser Cys Lys Phe Ile Ile Leu Val Pro Thr
 405 410 415
 Gln Cys Gly Ser Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Glu Lys
 420 425 430
 Met Ala Met Leu Glu Gln Asp Pro His Phe Leu Ala Leu Ala Ser Pro
 435 440 445
 Lys Thr Leu Ile
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 <223> partial cDNA

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 Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu
 1 5 10 15

gga ggt gtt gga cac atg ggg gtg aag ata gca aag gct atg gga cac 95
 Gly Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His
 20 25 30

cat atc acc gtg ata agc tct tct gat aag aag aaa aaa gag gcc ttg	143		
His Ile Thr Val Ile Ser Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu			
35	40	45	
gag cat att ggt gct gat gag tac ttg gtg agc tct gat gcc acc caa	191		
Glu His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln			
50	55	60	
atg caa gag gct atg gac tca ctg gat tac att att gac acc att cca	239		
Met Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro			
65	70	75	
gtg ttc cac cct ctt gag cct tac ctc tct ttg ttg aag ctt gat ggg	287		
Val Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly			
80	85	90	95
aag ttg atc ttg atg ggt gtt atc aac acc cca ttg caa ttt gtc tct	335		
Lys Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser			
100	105	110	
cca ttg gtc atg ctt ggg gag gaa gac gat cac cg ^g gag ctt tgt ggg	383		
Pro Leu Val Met Leu Gly Glu Glu Asp Asp His Arg Glu Leu Cys Gly			
115	120	125	
gag cat gaa gga gat gga gga gat gct cga gtt ctg caa aga gaa aga	431		
Glu His Glu Gly Asp Gly Asp Ala Arg Val Leu Gln Arg Glu Arg			
130	135	140	
gct gaa acg atg att gaa gtg gtg aag atg gac tac atc aac gaa gct	479		
Ala Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala			
145	150	155	
ttc gaa agg ttg gag aag aac gac gtt agg tac agg ttc gtt gtg gat	527		
Phe Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp			
160	165	170	175
tgt tgc cgg cag caa tct tgatcaataa gaaagaaaaga aggcatacatc	575		
Cys Cys Arg Gln Gln Ser			
180			
gagtgttgc ctattttat cgagtactct gtctcatctt atcttaaaca atataaataaa	635		
acaaaagaaaa aaaaaaaaaa aaaaaaaaa	663		
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 Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
 1 5 10 15

 tgt gaa gac gag ttt aaa aag ata atg aag ata aat ttc atg tct gca 96
 Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
 20 25 30

 tgg ttt ctg gta aat gcc gtt ggc aga aga atg cga gat cat aaa tca 144
 Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
 35 40 45

 gga ggt tcc atc ata ttg ttg acc tcg att gtt gga gct gaa aga ggg 192
 Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
 50 55 60

 ctt tat aca gga gct gtt gcc tat ggt gca tgc gca gca ctg cag 240
 Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
 65 70 75 80

 cag tta gta agg tcg tcg gca ttg gag att gga aaa tac cag atc agg 288
 Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
 85 90 95

 gtt aat gca atc gca cgt ggt ttg cat ttg gaa gat gag ttt cct aag 336
 Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
 100 105 110

 tct gtg gga ata gag aga gca aag aag ctg gtg aat gat gca gtt ccg 384
 Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
 115 120 125

 ctg gag aga tgg ctt gat gtt aaa aat gat gtg gct tca agt gtc ata 432
 Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
 130 135 140

 tat ttg gtc agt gat ggt tca agg tac atg acg ggc aca act ata ttt 480
 Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
 145 150 155 160

 gtt gat ggg gca cag tct ctc gtg agg cct cga atg cgt tct tat atg 528
 Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met
 165 170 175

 tgattcttgc tccttattata tcctccttagc cattattagc tacttaggtt tgttcatact 588
 tcataggtga actcatttagc tattcttaca tttgttcctt atgaataaag aagtcaagat 648
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 <210> 9
 <211> 1586
 <212> DNA
 <213> Fragaria x ananassa

<221> CDS
<222> (78) .. (1268)
<223> cDNA

<220>
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tgaatcgcaa tgccaaac atg gcc aag ctt caa gcc ggt tat ctt ttt cca 110
Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro
1 5 10
gag att gcg agg agg agg aat gcg cac ttg cag aag cac cct gat gcg 158
Glu Ile Ala Arg Arg Arg Asn Ala His Leu Gln Lys His Pro Asp Ala
15 20 25
aag ata att cca ctt gga att ggt gat act acc gag cca att cca gaa 206
Lys Ile Ile Pro Leu Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu
30 35 40
tat ata acc tct gca atg gca aag aga gca ctt gcc atg tcc acc cta 254
Tyr Ile Thr Ser Ala Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu
45 50 55
gag ggt tac agt ggt tat gga cct gaa caa ggt gaa aag cca ctg aga 302
Glu Gly Tyr Ser Gly Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg
60 65 70 75
gtt gca att gct aaa acg ttt tat ggc gac ctt ggc ata gag gaa gat 350
Val Ala Ile Ala Lys Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp
80 85 90
gac ata ttt gtt tct gat ggg gca aaa tgt gac ata tcc cgc ctt cag 398
Asp Ile Phe Val Ser Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln
95 100 105
gtt ctt ttt ggg gcg gat aaa aca ata gca gtg caa gat cca tcg tat 446
Val Leu Phe Gly Ala Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr
110 115 120
ccg gct tat gta gac tca agt gtt att atg ggc cag aca gga cag tat 494
Pro Ala Tyr Val Asp Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr
125 130 135
cag aaa tct gtt cag aag ttt gga aac atc gag tac atg agg tgt act 542
Gln Lys Ser Val Gln Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr
140 145 150 155
ccc gat aat gga ttt ttt cct gat ctg tcc tct act aag cga aca gat 590
Pro Asp Asn Gly Phe Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp
160 165 170
atc ata ttt ttc tgt tca cca aac aat cct act ggt tct gct gca aca 638
Ile Ile Phe Phe Cys Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr
175 180 185

agg gag caa ctg aca caa ctt gta aag ttt gcc aag gat aat ggt tca	686		
Arg Glu Gln Leu Thr Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser			
190	195	200	
atc ata gtc tat gat tct gca tat gcc atg tat atg tca gat gat aat	734		
Ile Ile Val Tyr Asp Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn			
205	210	215	
cca cgc tcc atc ttt gaa atc cct gga gct aaa gat gtt gca ctt gag	782		
Pro Arg Ser Ile Phe Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu			
220	225	230	235
aca tca tca ttt agt aag tat gcc gga ttc act gga gtt cgt ttg ggg	830		
Thr Ser Ser Phe Ser Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly			
240	245	250	
tgg act gtg gtt cca aag cag ttg cag tat tca gat ggt ttt caa gtt	878		
Trp Thr Val Val Pro Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val			
255	260	265	
gcc aag gat ttc aac cgc att gtt tgt act tgc ttc aat ggt gca tcc	926		
Ala Lys Asp Phe Asn Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser			
270	275	280	
act att atc caa gct ggt ctg gct tgc ctt caa cca aag ggt gtt	974		
Thr Ile Ile Gln Ala Gly Leu Ala Cys Leu Gln Pro Lys Gly Val			
285	290	295	
aag gct atg cac ggt gtg ata aat ttc tac aaa gaa aat act aag atc	1022		
Lys Ala Met His Gly Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile			
300	305	310	315
ata atg gag acg ttt aac tct ctt ggc ttt aac gtg tat gga ggg aca	1070		
Ile Met Glu Thr Phe Asn Ser Leu Gly Phe Asn Val Tyr Gly Thr			
320	325	330	
aac gct cca tat gtg tgg gtc cac ttc cct gga caa agc tcc tgg gat	1118		
Asn Ala Pro Tyr Val Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp			
335	340	345	
gtg ttt gct gag atc ctt gag aag act cat gtg gta acc aca cct gga	1166		
Val Phe Ala Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly			
350	355	360	
agt ggc ttt gga cct ggt ggt gaa ggt ttc atc agg gta agt gcc ttt	1214		
Ser Gly Phe Gly Pro Gly Glu Gly Phe Ile Arg Val Ser Ala Phe			
365	370	375	
gga cac agg aaa aat ata tta gaa gca tgt aaa aga ttc aag caa tta	1262		
Gly His Arg Lys Asn Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu			
380	385	390	395
tac aag tgaggactgc ggatctgaat tgttagaccag tttctactgc atgctagttg	1318		
Tyr Lys			
aacctatttg cctccattt ccgttctatg ctaaatattt tagcacgttc caattccgta	1378		

ttcagttgt cggcttagt ttatgaatta tggagattt agctattgta aaaatgattc 1438
 gatcagcctt gtttcatgt gttacacta attgtttaa catttgcgt gatcagaagc 1498
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 gcctgcaaaa aaaaaaaaaa aaaaaaaaaa 1586

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 1 5 10 15

cca gca aat cct aca ccc tat gaa ttt aaa caa ctt tct gat gtg gat 96
 Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
 20 25 30

gat caa caa agc tta agg ctt caa ttg cca ttc gta aat atc tat ccc 144
 Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
 35 40 45

cat aat cca agt ttg gag gga aga gat cca gtg aag gta ata aag gaa 192
 His Asn Pro Ser Leu Glu Gly Arg Asp Pro Val Lys Val Ile Lys Glu
 50 55 60

gca att gga aag gcg ttg gtg ttc tac tat cct tta gca gga aga ttg 240
 Ala Ile Gly Lys Ala Leu Val Phe Tyr Tyr Pro Leu Ala Gly Arg Leu
 65 70 75 80

aga gaa ggg cca ggt aga aag ctt ttt gtt gaa tgt aca ggt gaa gga 288
 Arg Glu Gly Pro Gly Arg Lys Leu Phe Val Glu Cys Thr Gly Glu Gly
 85 90 95

atc ttg ttt att gaa gcg gat gca gat gtg agc tta gaa gaa ttt tgg 336
 Ile Leu Phe Ile Glu Ala Asp Ala Asp Val Ser Leu Glu Glu Phe Trp
 100 105 110

gat act ctt cca tat tca ctt tca agc atg cag aac aat att ata cat 384
 Asp Thr Leu Pro Tyr Ser Leu Ser Ser Met Gln Asn Asn Ile Ile His
 115 120 125

aac gct tta aat tct gat gaa gtc ctc aat tct cca tta ttg ctc att 432
 Asn Ala Leu Asn Ser Asp Glu Val Leu Asn Ser Pro Leu Leu Ile

130	135	140														
cag	gtg	aca	cga	ctc	aag	tgt	gga	ggt	ttc	att	ttt	ggt	ctt	tgt	ttc	480
Gln	Val	Thr	Arg	Leu	Lys	Cys	Gly	Gly	Phe	Ile	Phe	Gly	Leu	Cys	Phe	
145				150						155				160		
aat	cat	act	atg	gca	gat	ggt	ttt	ggt	att	gtc	caa	ttc	atg	aag	gct	528
Asn	His	Thr	Met	Ala	Asp	Gly	Phe	Gly	Ile	Val	Gln	Phe	Met	Lys	Ala	
				165					170				175			
aca	gct	gag	ata	gct	cgt	gga	gct	ttt	gct	cca	tct	att	tta	cca	gta	576
Thr	Ala	Glu	Ile	Ala	Arg	Gly	Ala	Phe	Ala	Pro	Ser	Ile	Leu	Pro	Val	
				180					185				190			
tgg	caa	aga	gct	ctc	tta	acc	gca	aga	gac	cct	ccc	aga	atc	act	ttt	624
Trp	Gln	Arg	Ala	Leu	Leu	Thr	Ala	Arg	Asp	Pro	Pro	Arg	Ile	Thr	Phe	
				195					200				205			
cgc	cac	tat	gaa	tac	gac	caa	gta	gtc	gac	atg	aag	agc	ggc	ctc	att	672
Arg	His	Tyr	Glu	Tyr	Asp	Gln	Val	Val	Asp	Met	Lys	Ser	Gly	Leu	Ile	
				210					215				220			
cca	gtc	aat	agc	aag	atc	gat	caa	tta	ttc	ttc	ttt	agc	caa	ctt	caa	720
Pro	Val	Asn	Ser	Lys	Ile	Asp	Gln	Leu	Phe	Phe	Ser	Gln	Leu	Gln		
				225					230				235		240	
atc	tcc	acc	ctt	cgc	caa	act	ttg	cca	gcc	cac	ctt	cac	gat	tgc	cct	768
Ile	Ser	Thr	Leu	Arg	Gln	Thr	Leu	Pro	Ala	His	Leu	His	Asp	Cys	Pro	
				245					250				255			
tcc	ttc	gag	gtc	ctc	act	gcc	tat	gtt	tgg	cgc	ctc	cgt	acc	ata	gcc	816
Ser	Phe	Glu	Val	Leu	Thr	Ala	Tyr	Val	Trp	Arg	Leu	Arg	Thr	Ile	Ala	
				260					265				270			
ctt	caa	ttt	aag	cca	gag	gag	gaa	gtg	cgg	ttt	ctt	tgc	gta	atg	aat	864
Leu	Gln	Phe	Lys	Pro	Glu	Glu	Val	Arg	Phe	Leu	Cys	Val	Met	Asn		
				275					280				285			
cta	cgc	tcg	aag	atc	gac	ata	cca	tta	ggg	tat	tat	ggt	aat	gct	gta	912
Leu	Arg	Ser	Lys	Ile	Asp	Ile	Pro	Leu	Gly	Tyr	Tyr	Gly	Asn	Ala	Val	
				290					295				300			
gtt	gtt	cct	gca	gtt	atc	acc	acc	gct	gct	aag	ctt	tgt	ggg	aac	cca	960
Val	Val	Pro	Ala	Val	Ile	Thr	Thr	Ala	Ala	Lys	Leu	Cys	Gly	Asn	Pro	
				305					310				315		320	
ctt	ggt	tat	gct	gta	gac	ttg	att	agg	aag	gcc	aag	gct	aag	gca	acg	1008
Leu	Gly	Tyr	Ala	Val	Asp	Leu	Ile	Arg	Lys	Ala	Lys	Ala	Lys	Ala	Thr	
				325					330				335			
atg	gag	tac	ata	aag	tct	acg	gtg	gat	ctt	atg	gtg	att	aaa	gga	cga	1056
Met	Glu	Tyr	Ile	Lys	Ser	Thr	Val	Asp	Leu	Met	Val	Ile	Lys	Gly	Arg	
				340					345				350			
ccc	tat	ttc	act	gta	gtt	gga	tca	ttt	atg	atg	tca	gac	cta	acg	aga	1104
Pro	Tyr	Phe	Thr	Val	Val	Gly	Ser	Phe	Met	Met	Ser	Asp	Leu	Thr	Arg	
				355					360				365			

att ggg gtt gaa aac gtg gac ttt gga tgg gga aag gcc att ttt gga		1152
Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly		
370	375	380
gga cct aca acc aca ggg gcc aga att aca cga ggt ttg gta agc ttt		1200
Gly Pro Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe		
385	390	395
400		
tgt gta cct ttc atg aat aga aat gga gaa aag gga act gcg tta agt		1248
Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser		
405	410	415
cta tgc ttg cct cct cca gcc atg gaa aga ttt agg gca aat gtt cat		1296
Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His		
420	425	430
gcc tcg ttg caa gtg aaa caa gtg gtt gat gca gtt gat agc cat atg		1344
Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met		
435	440	445
caa act att caa tct gct tcg aaa taaataatat tggtgaaggt gggctgaggt		1398
Gln Thr Ile Gln Ser Ala Ser Lys		
450	455	
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1	5	10
		15
act ccg gca aag tca acg cct caa gaa aca aag ttt ctc tca gat att		96
Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile		
20	25	30
gac gac caa gaa agc ttg aga gtt cag att cca atc ata atg tgt tac		144

Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr				
35	40	45		
aaa gac aac cct tca ctt aat aaa aat cgt aat ccc gtt aag gca att				192
Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile				
50	55	60		
agg gaa gcc tta agt aga gca tta gtg tat tac tac ccc tta gct gga				240
Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly				
65	70	75		80
agg ctt agg gaa ggg cct aat aga aag ctc gtg gtc gat tgc aat ggt				288
Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly				
85	90	95		
gaa ggt atc ttg ttc gtt gag gct tct gct gat gtc aca ctt gag caa				336
Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln				
100	105	110		
cta gga gac aaa att cta ccc cct tgt cca ctt tta gag gag ttc tta				384
Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu				
115	120	125		
tat aat ttt cca ggc tct gat gga att att gat tgt cct ttg ctg ctg				432
Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu				
130	135	140		
att cag gtg acc tgt ctt aca tgt gga ggt ttc ata ctt gca ttg cgc				480
Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg				
145	150	155		160
cta aac cac aca atg tgt gat gca gct gga ttg ctc ttg ttc ctg acc				528
Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr				
165	170	175		
gcc atc gcg gag atg gca aga ggc gca cat gca cca tct att cta cca				576
Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro				
180	185	190		
gtg tgg gag aga gag ctc ttg ttc gct cga gat cca cca aga att aca				624
Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr				
195	200	205		
tgt gct cgt cat gaa tat gaa gac gtg att ggt cat tct gat ggc tca				672
Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser				
210	215	220		
tac gca tcc agt aac cag tca aac atg gtt caa cga tct ttg tac ttt				720
Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe				
225	230	235		240
ggt gcc aag gag atg aga gtc ctt cga aaa cag att cca ccc cac cta				768
Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu				
245	250	255		
att tcc act tgc tcc aca ttt gac ttg atc aca gct tgt ttg tgg aaa				816
Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys				

260	265	270	
tgt cgc act ctt gca ctt aac att aat cca aaa gag gct gtt cga gtt			864
Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val			
275	280	285	
tca tgc att gtc aat gca cga gga aag cac aac aat gta cgt ctt ccc			912
Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro			
290	295	300	
ttg gga tac tat ggc aat gca ttt gca ttt cca gct gca att tcg aag			960
Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys			
305	310	315	320
gct gaa cct cta tgc aaa aat cca ctg gga tat gct ttg gag ttg gtg			1008
Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val			
325	330	335	
aag aag gct aaa gct acc atg aat gaa gaa tac tta aga tca gtg gca			1056
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala			
340	345	350	
gat ctt ttg gta cta aga ggg cga cct caa tat tca tcg aca gga agt			1104
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser			
355	360	365	
tat tta ata gtt tct gat aat acg cgt gta ggt ttt gga gat gtc aat			1152
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn			
370	375	380	
ttt gga tgg gga cag ccg gta ttt gct gga ccc gtc aag gcc ttg gat			1200
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp			
385	390	395	400
ttg att agc ttc tac gtt caa cac aaa aac aac aca gag gat gga ata			1248
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile			
405	410	415	
ttg gta cca atg tgt ttg cca tcc tcg gcc atg gag aga ttt cag cag			1296
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln			
420	425	430	
gaa cta gag agg att act cag gaa cct aag gag gat ata tgt aac aac			1344
Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn			
435	440	445	
ctt aga tca act agt caa tgatgtaagt gttaaacgtatgcactttc			1392
Leu Arg Ser Thr Ser Gln			
450			
tgtatgtat agttgtgtct cttggactt atcncaagag ttatagctgt tatccaaagg			1452
tctgaatgtt attaaaaat agccaaataat aag			1485
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<212> DNA			
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<223> cDNA

<220>
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<400> 12
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Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys
1 5 10 15
g^{gg} g^{tc} a^{cg} c^{cg} a^{cg} g^{gc} t^{cg} c^{tc} g^{gc} c^{tc} t^{cc} g^{cc} a^{tc} g^{ac} c^{gg} g^{tg} 96
Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
20 25 30
c^{cc} g^{gc} c^{tc} a^{gg} c^{at} a^{tg} g^{tg} c^{gg} t^{cg} c^{ta} c^{ac} g^{tg} t^{tc} a^{gg} c^{aa} g^{gc} 144
Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
35 40 45
c^{gg} g^{ag} c^{cg} g^{cc} a^{gg} a^{tc} a^{tc} a^{gg} g^{aa} g^{ca} c^{tg} t^{cg} a^{ag} g^{cg} c^{tg} g^{tg} 192
Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
50 55 60
a^{ag} t^{ac} t^{ac} c^{cc} t^{tc} g^{cg} g^{gg} c^{gg} t^{tc} g^{tg} g^{ac} g^{at} c^{cc} g^{ag} g^{gc} g^{gc} 240
Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
65 70 75 80
g^{gc} g^{ag} g^{tt} c^{gt} g^{tc} g^{ct} t^{gc} a^{ct} g^{gc} g^{ag} g^{gc} g^{ct} t^{gg} t^{tc} g^{tc} g^{ag} 288
Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
85 90 95
g^{cc} a^{ag} g^{cg} g^{ac} t^{gc} a^{gc} t^{tg} g^{ag} g^{ac} g^{tg} a^{ag} t^{ac} c^{tc} g^{at} c^{tc} c^{cg} 336
Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
100 105 110
c^{tc} a^{tg} a^{tc} c^ct g^{ag} g^{ac} g^{cg} c^{tc} c^{tg} c^{cc} a^{ag} c^{cc} t^{gc} c^{cg} g^{ga} c^{tg} 384
Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
115 120 125
a^{ac} c^{cc} c^{tc} g^{ac} c^{tc} c^{tc} a^{tg} c^{tg} c^{ag} g^{tg} a^{ca} g^{ag} t^{tc} g^{tg} g^{gc} 432
Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
130 135 140
g^{gc} g^{ga} t^{tc} g^{tg} g^{tc} g^{gc} c^{tc} a^{tc} t^{cc} g^{tc} c^{at} a^{cc} g^{cc} g^{ac} g^{gc} 480
Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
145 150 155 160
c^{tc} g^{gc} g^{tc} c^{ag} t^{tc} a^{tc} a^{ac} g^{cc} g^{tc} g^{cc} g^{ag} a^{tc} g^{cc} c^{gt} g^{gc} 528
Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
165 170 175
c^{tg} c^{cg} a^{ag} c^{cc} a^{cc} g^{tg} g^{ag} c^ct g^{ca} t^{gg} t^{cc} c^{gg} g^{ag} g^{tc} a^{ta} c^{cc} 576
Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
180 185 190

aac cca cct aag ctg cct ccc ggt ggc ccg ccc gtg ttc ccc tcc ttc		624	
Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe			
195	200	205	
aag ctg ctc cac gcc acc gtc gac cta tcc cct gac cac atc gat cac		672	
Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His			
210	215	220	
gtc aag tcc cga cac ttg gag ctc acc ggc cag cgc tgc tct acc ttc		720	
Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe			
225	230	235	240
gac gtc gcc atc gcc aac ctg tgg cag tcc cgc acg cgc gcc atc aac		768	
Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn			
245	250	255	
ctg gac cca ggc gtc gac gtg cac gtg tgc ttc ttc gcc aac act cgc		816	
Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg			
260	265	270	
cac ctg ttg cgc cag gtc ctc ctg ccc ccc gag gat ggc tac tac		864	
His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr			
275	280	285	
ggc aac tgc ttc tac ccg gtg acc gcc acc gcc cca agc ggc agg atc		912	
Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile			
290	295	300	
gca tcg gcc gag ctc atc gat gtc gtc agc atc atc agg gac gcc aag		960	
Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys			
305	310	315	320
tcg agg ctg ccg ggc gag ttc gcc aag tgg gct gcc ggg gat ttc aag		1008	
Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys			
325	330	335	
gac gac cct tac gag ctc agc ttc acg tac aac tcg ctg ttc gtg tcg		1056	
Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser			
340	345	350	
gac tgg acc cgg ctc ggc ttc ctc gac gtc gac tac ggc tgg ggc aag		1104	
Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys			
355	360	365	
ccc ctc cac gtt ata ccg ttc gcg tac ttg gac atc atg gcg gtc ggc		1152	
Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly			
370	375	380	
atc atc ggg gcg ccg ccg gcg cca aag ggg act cgg gtg atg gcg		1200	
Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala			
385	390	395	400
cag tgc gtc gag aag gag cac atg cag gcg ttc ctg gaa gag atg aaa		1248	
Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys			
405	410	415	
ggc ttc gct taaaccagca gcagtgttagt acttgtcagt atcc		1291	

Gly Phe Ala

<210> 13

<211> 1488

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<213> Fragaria vesca

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<221> CDS

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<223> cDNA

<220>

<223> Strawberry vesca alcohol acyl transferase

<400> 13

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Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro	
1 5 10 15	

tca act tcc tct tca cca ctt cag cct tac aag ctt acc ctg ctc gac	96
Ser Thr Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp	
20 25 30	

cag ctc act cct cca tcg tat gtc ccc atg gta ttc ttc tac ccc att	144
Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile	
35 40 45	

act ggc cct gca gtc ttc aat ctt caa acc cta gct gac tta aga cat	192
Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His	
50 55 60	

gcc ctt tcc gag act ctc act ttg tac tat cca ctc tct gga agg gtc	240
Ala Leu Ser Glu Thr Leu Thr Tyr Tyr Pro Leu Ser Gly Arg Val	
65 70 75 80	

aaa aac aac cta tac atc gat gat ttt gaa gag ggt gtc cca tac ctt	288
Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu	
85 90 95	

gag gct cga gtg aac tgt gac atg aat gat ttt cta agg ctt ccg aaa	336
Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys	
100 105 110	

atc gag tgc cta aat gag ttt gtt cca ata aaa cca ttt agt atg gaa	384
Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu	
115 120 125	

gca ata tct gat gag cgt tac cct ttg ctc gga gtt caa gtt aac att	432
Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile	
130 135 140	

ttc aac tcc gga ata gca atc ggg gtc tcc gtc tct cac aag ctc atc	480
Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile	
145 150 155 160	

gat gga aga act tca gac tgt ttt ctc aag tcg tgg tgt gct gtt ttt	528
Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe	

165	170	175	
cgt ggt tct cgt gac aaa atc ata cat cct aat ctc tct caa gca gca Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala			576
180	185	190	
ttg ctt ttc cca cca aga gat gac ttg cct gaa aag tat gcc cgt cag Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln			624
195	200	205	
atg gaa ggg tta tgg ttt gtc gga aaa aaa gtt gct aca agg aga ttt Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe			672
210	215	220	
gta ttt ggt gcg aaa gcc ata tct gta att caa gat gaa gca aag agc Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser			720
225	230	235	240
gag tcc gtg ccc aag cca tca cga gtt cag gct gtc act agt ttt ctc Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu			768
245	250	255	
tgg aaa cat cta atc gct act tct cgg gca cta aca tca ggt act act Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr			816
260	265	270	
tca aca aga ctt tct ata gca acc cag gta gtg aac ata aga tca cgg Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg			864
275	280	285	
agg aac atg gag aca gtg tgg gat aat gcc att gga aac ttg ata tgg Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp			912
290	295	300	
ttc gct ccg gcc ata cta gag cta agt cat aca aca cta gag atc agt Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser			960
305	310	315	320
gat ctt aag ctg tgt gac ttg gtt aac ttg ctc aat gga tct gtc aaa Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys			1008
325	330	335	
caa tgt aac ggt gat tac ttt gag act ttc atg ggt aaa gag gga tat Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr			1056
340	345	350	
gga agc atg tgc gag tat cta gat ttt cag agg act atg agt tct atg Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met			1104
355	360	365	
gaa cca gca cca gag att tat tta ttc acg agc tgg act aat ttt ttc Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe			1152
370	375	380	
aac caa ctt gat ttt gga tgg ggg agg aca tca tgg att gga gtt gca Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala			1200
385	390	395	400

gga aaa att gaa tct gca ttt tgc aat ctc aca aca tta gtt cca aca	405	410	415	1248
Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr				
cca tgc gat act gga att gaa gcg tgg gtg aat cta gaa gaa gaa aaa	420	425	430	1296
Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Lys				
atg gct atg cta gaa caa gat ccc cag ttt cta gca cta gca tct cca	435	440	445	1344
Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro				
aag acg cta att tca aga tat tgattaagga agattatgcg gctcgtgcaa	450	455		1395
Lys Thr Leu Ile Ser Arg Tyr				
tgtttccatt ttgttgtat taaggcttaa attagttcac cagccaatca ataagatgca				1455
agtatgatag actcggtcta cgtatgttat ccg				1488
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<400> 14				
Met Lys Ile His Val Lys Glu Ser Thr Ile Ile Arg Pro Ala Gln Glu	1	5	10	15
Thr Pro Lys His Arg Leu Gln Ile Ser Asp Leu Asp Met Ile Val Pro	20	25	30	
Ser Asn Tyr Val Pro Ser Val Tyr Phe Tyr Arg Arg Ser Ser Asp Cys	35	40	45	
Thr Asp Phe Phe Glu Val Gly Leu Leu Lys Ala Leu Ser Glu Val	50	55	60	
Leu Val Pro Phe Tyr Pro Val Ala Gly Arg Leu Gln Lys Asp Glu Asn	65	70	75	80
Arg Lys Ile Glu Ile Leu Cys Asn Gly Glu Gly Val Leu Phe Leu Glu	85	90	95	
Ala Glu Thr Ser Cys Gly Ile Asp Asp Phe Gly Asp Phe Ser Gln Gly	100	105	110	
Ser Lys Leu Leu Thr Leu Val Pro Thr Val Gly Asp Thr Lys Asp Ile	115	120	125	
Ser Ser His Pro Leu Leu Met Ala Gln Val Thr Tyr Phe Lys Cys Gly	130	135	140	

Gly Val Cys Val Gly Thr Arg Val Asn His Thr Leu Val Asp Gly Ala
 145 150 155 160
 Ser Ala Tyr His Ile Ile Asn Ser Trp Ala Glu Thr Thr Arg Gly Val
 165 170 175
 Pro Ile Ser Thr Gln Pro Phe Tyr Asp Arg Thr Ile Leu Ser Val Gly
 180 185 190
 Val Pro Thr Ser Pro Lys Phe His His Ile Glu Tyr Asp Pro Pro Pro
 195 200 205
 Ser Met Asn Ala Pro Pro Thr Gln Asn Pro Glu Ile Ile Ser Thr Ala
 210 215 220
 Ile Leu Asn Leu Ser Leu Asp Gln Ile His Thr Leu Lys Glu Lys Ser
 225 230 235 240
 Lys Thr Asp His Glu Pro Asn Val Lys Tyr Ser Arg Met Ala Ile Leu
 245 250 255
 Ala Ala His Ile Trp Arg Ser Met Cys Lys Ala Arg Gly Leu Ser Asp
 260 265 270
 Asp Gln Val Ser Lys Leu His Phe Pro Thr Asp Gly Arg Gln Arg Leu
 275 280 285
 Asn Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Thr
 290 295 300
 Ser Leu Thr Ala Ser Ser Gly Asp Ile Leu Ser Glu Pro Leu Asn His
 305 310 315 320
 Thr Val Glu Arg Ile Gln Lys Ala Leu Lys Arg Met Asp Asp Glu Tyr
 325 330 335
 Leu Lys Ser Ala Leu Ala Tyr Leu Lys Gln Gln Pro Asp Leu Asn Ala
 340 345 350
 Leu Arg Lys Gly Gly His Ile Tyr Lys Cys Pro Asn Leu Asn Ile Val
 355 360 365
 Asn Leu Ala Asn Met Pro Met Tyr Val Ala Asn Phe Gly Trp Gly Gln
 370 375 380
 Pro Ile Phe Ala Arg Ile Val Asn Thr Tyr Tyr Glu Gly Ile Ala His
 385 390 395 400
 Ile Tyr Pro Ser Pro Ser Asn Asp Gly Thr Leu Ser Val Val Ile Asn
 405 410 415
 Ser Val Ala Asp His Met Gln Leu Phe Lys Lys Phe Phe Tyr Glu Ile
 420 425 430
 Phe Asp

<210> 15
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<212> DNA

<213> Mangifera indica

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<221> CDS

<222> (1)..(1293)

<223> cDNA

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1 5 10 15

acg ccg agg ata tct ctg tgg aac tcc aac gcc gat ctg gtg gtt ccc 96
Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro
20 25 30

cga ttt cat act ccc agc gtt tac ttc tac ccg ccc acc ggg gcc ata 144
Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile
35 40 45

aac ttc ttt gat ggt aag ttg ctc aag gag gct ctc ggc aag gct ctg 192
Asn Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu
50 55 60

gtg ccg ttc tac cca atg gcg ggg ccg tta aag cgt gac gaa gat gga 240
Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly
65 70 75 80

agg att gag atc gat tgt aat gct gaa ggc gtc ttg ttt gtt gag gcc 288
Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala
85 90 95

gaa act ccc tct gtt att gat gat ttt ggt gac ttt gcg ccc act tta 336
Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu
100 105 110

gag ctc aag cag ctc att ccg aca gtg gat tac tcc ggc ggg atc tct 384
Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser
115 120 125

acg tat ccc cta ttg gcg tta cag gtt act cac ttc aaa tgt ggt gga 432
Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly
130 135 140

gtt tca ctt ggt gta ggt atg caa cac cat gcg gca gat gga ttt tct 480
Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser
145 150 155 160

ggt ctt cac ttt gta aac aca tgg tca gac att gct cgt ggt ctt gat 528
Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp
165 170 175

gtt aac atc acc ctg ttc att gac ccg act ctc aga gca cag gat 576

Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp			
180	185	190	
ccc cct cag cct act ttc cca cac aca tgg aat acc agg ccg cct cct			624
Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro			
195	200	205	
tcc ctg aaa act cct cca cca gca gtt tct gag cct act gct gtc tcc			672
Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser			
210	215	220	
att ttt aag ttg acg cgg gac cag ctc aac atc ctc aaa gcc aag gcc			720
Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala			
225	230	235	240
aaa gaa gat ggt aac act atc aac tat agc tca tat gag atg ctg gcg			768
Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala			
245	250	255	
ggt cat gtc tgg aga tct gca tgc aag gca cgc ggc tta tct gat gat			816
Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp			
260	265	270	
caa gag act aaa ttg tac ata gca act gac gga cgt gct aga tta atc			864
Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile			
275	280	285	
ccc cca ctt cca cct ggt tac ttt ggg aat gtg ata ttt aca gcc aca			912
Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr			
290	295	300	
cca atg gca gta gca ggt gat ctc cag tca aag cct ata tgg tat gct			960
Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala			
305	310	315	320
gct ggc cag att cat gat gcc ttg gtt cga atg gac aac gac tat tta			1008
Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu			
325	330	335	
agg tca gcc ctc gat tac cta gag ctt cag cct gat tta tca gca tta			1056
Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu			
340	345	350	
gtt cgt ggt gcc cat aca ttt agg tgt cca aat ctc ggg att act agt			1104
Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser			
355	360	365	
tgg gtt aga ctg cca ata cat gat gca gat ttt ggt tgg ggt cca ccc			1152
Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro			
370	375	380	
aca ttt atg ggg cct ggt ggg att gca tat gaa ggc tta tca ttt gta			1200
Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val			
385	390	395	400
ttg cca agc cct aca aat gat ggg agc tta tca gtt gcc atc tct cta			1248
Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu			
405	410	415	

140	145	150	
cac aaa gtt att gat gca aca acg gct gca ttc ttt gtt aag aac tgg			534
His Lys Val Ile Asp Ala Thr Thr Ala Ala Phe Phe Val Lys Asn Trp			
155	160	165	
ggt gta att gct cgt ggt gct gga gaa att aag gac gtg atc att gat			582
Gly Val Ile Ala Arg Gly Ala Gly Glu Ile Lys Asp Val Ile Ile Asp			
170	175	180	
cat gct tcc ctg ttt ccc gca aga gat tta tcg tgc tta aca aag agt			630
His Ala Ser Leu Phe Pro Ala Arg Asp Leu Ser Cys Leu Thr Lys Ser			
185	190	195	
gtt gac gaa gag ttt ttg aag cca gag tct gaa aca aag cgc ttt gtg			678
Val Asp Glu Glu Phe Leu Lys Pro Glu Ser Glu Thr Lys Arg Phe Val			
200	205	210	215
ttt gat ggt gcc act ata gct tct tta caa gaa acg ttt gca agt ttt			726
Phe Asp Gly Ala Thr Ile Ala Ser Leu Gln Glu Thr Phe Ala Ser Phe			
220	225	230	
gaa cga cgt cca aca cgc ttt gag gtt gtg tca gca gtt att ttg ggt			774
Glu Arg Arg Pro Thr Arg Phe Glu Val Val Ser Ala Val Ile Leu Gly			
235	240	245	
gct ttg ata act gca acg aga gaa tct gat gat gag tct aac gtt cct			822
Ala Leu Ile Thr Ala Thr Arg Glu Ser Asp Asp Glu Ser Asn Val Pro			
250	255	260	
gaa cgt ttg gac acg ata att tca gtg aat cta cgg cag aga atg aat			870
Glu Arg Leu Asp Thr Ile Ile Ser Val Asn Leu Arg Gln Arg Met Asn			
265	270	275	
cca cca ttc ccg gag cat tgc atg ggg aat ata ata tcc ggg gga tta			918
Pro Pro Phe Pro Glu His Cys Met Gly Asn Ile Ile Ser Gly Gly Leu			
280	285	290	295
gtg tat tgg cca ctg gag aaa aaa gtt gat tac ggg tgt tta gca aaa			966
Val Tyr Trp Pro Leu Glu Lys Lys Val Asp Tyr Gly Cys Leu Ala Lys			
300	305	310	
gag att cat gaa tca ata aag aaa gtg gac gat caa ttt gcg agg aag			1014
Glu Ile His Glu Ser Ile Lys Lys Val Asp Asp Gln Phe Ala Arg Lys			
315	320	325	
ttc tat ggg gac gca gag ttc ttg aac ctg ccg agg ctt gcg ggt gct			1062
Phe Tyr Gly Asp Ala Glu Phe Leu Asn Leu Pro Arg Leu Ala Gly Ala			
330	335	340	
gag gat gtg aag aag cgg gag ttt tgg gtt act agt tgg tgc aaa act			1110
Glu Asp Val Lys Lys Arg Glu Phe Trp Val Thr Ser Trp Cys Lys Thr			
345	350	355	
ccg ctg tat gaa gct gat ttc ggg tgg ggg aat cct aag tgg gca ggc			1158
Pro Leu Tyr Glu Ala Asp Phe Gly Trp Gly Asn Pro Lys Trp Ala Gly			
360	365	370	375

aac tcc atg agg ctt aat cag att act gtt ttc ttt gac agt agt gat 1206
Asn Ser Met Arg Leu Asn Gln Ile Thr Val Phe Phe Asp Ser Ser Asp
380 385 390

ggt gag gga gtt gaa gct tgg gtg ggg ttg ccc aga aaa gac atg gct 1254
Gly Glu Gly Val Glu Ala Trp Val Gly Leu Pro Arg Lys Asp Met Ala
395 400 405

cga ttt gaa aaa gat tct ggc atc ctt gct tac act tcc cct aat cca 1302
Arg Phe Glu Lys Asp Ser Gly Ile Leu Ala Tyr Thr Ser Pro Asn Pro
410 415 420

agc ata ttt tgagggtta tttatTTTTT attgcactgt ttgttatttg 1351
Ser Ile Phe
425

tactggcttg ctggAACAT attctggCAA atttcgCTGA tgcaAGTATC attctCCATA 1411
aaaatgtcaa aaaaaaaaaaaa aaaaaa 1436

<210> 17
<211> 1648
<212> DNA
<213> Citrus limon

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<223> cDNA

<220>
<223> Lemon acyl transferase

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Met Ala
1

gca att gaa aac aga gta aca cta aag aag cat gag gtt acc aaa gtc 105
Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr Lys Val
5 10 15

acc cct ttc gtc aac ccc aac tca aag acg acg tcg ttt act ctc gat 153
Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr Leu Asp
20 25 30

ctc acc tat ttc gac ttt ttc tgg ttc aag aat cct cct gtg gaa cgc 201
Leu Thr Tyr Phe Asp Phe Phe Trp Phe Lys Asn Pro Pro Val Glu Arg
35 40 45 50

ctc ttc ttc tat gag atg act gac ttg acg tgg gat tta ttc aac tcg 249
Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe Asn Ser
55 60 65

gag atc ctc cca aag ctg aag cac tcc ctt tcc ttc act ctc ctt cat 297

Glu	Ile	Leu	Pro	Lys	Leu	Lys	His	Ser	Leu	Ser	Phe	Thr	Leu	Leu	His	
70															80	
tac ctc cct ctt gct ggt cac atc atg tgg ccg ctg gat gcc gca aag															345	
Tyr	Leu	Pro	Leu	Ala	Gly	His	Ile	Met	Trp	Pro	Leu	Asp	Ala	Ala	Lys	
85															95	
cct gcc gtc tac tac ttt ccc gac caa aac gac ggc gtt tca ttc gca															393	
Pro	Ala	Val	Tyr	Tyr	Phe	Pro	Asp	Gln	Asn	Asp	Gly	Val	Ser	Phe	Ala	
100															110	
gtt gct gag tgg tct tcc gag tgc cac gca ggc ttc cat cac ctc tcc															441	
Val	Ala	Glu	Trp	Ser	Ser	Glu	Cys	His	Ala	Gly	Phe	His	His	Leu	Ser	
115															130	
ggc aac gga atc cgc caa gca gtt gaa ttt cat cct ctt gtg ccc cag															489	
Gly	Asn	Gly	Ile	Arg	Gln	Ala	Val	Glu	Phe	His	Pro	Leu	Val	Pro	Gln	
135															145	
ttg tcg ctt acg gac gat aaa gct gag gta att gcc atc caa ata aca															537	
Leu	Ser	Leu	Thr	Asp	Asp	Lys	Ala	Glu	Val	Ile	Ala	Ile	Gln	Ile	Thr	
150															160	
ctg ttt ccg aat caa ggc ttc tca att ggt gtt tca tct cac cat gca															585	
Leu	Phe	Pro	Asn	Gln	Gly	Phe	Ser	Ile	Gly	Val	Ser	Ser	His	His	Ala	
165															175	
att ctt gat gga aaa act tcg acc ttg ttc ctg aaa tct tgg gct tat															633	
Ile	Leu	Asp	Gly	Lys	Thr	Ser	Thr	Leu	Phe	Leu	Lys	Ser	Trp	Ala	Tyr	
180															190	
ttg tgc aaa caa tta caa tta tgc cat cac cct tgt ttg tca cct gaa															681	
Leu	Cys	Lys	Gln	Leu	Gln	Leu	Cys	His	His	Pro	Cys	Leu	Ser	Pro	Glu	
195															210	
cta acc cct ctt ctc gac cgg act gtc atc aaa gat ccg aca ggt cag															729	
Leu	Thr	Pro	Leu	Leu	Asp	Arg	Thr	Val	Ile	Lys	Asp	Pro	Thr	Gly	Gln	
215															225	
gac atg ctg caa ctg aat aag tgg gtt gtc ggg tcg gat aat tcg gat															777	
Asp	Met	Leu	Gln	Leu	Asn	Lys	Trp	Val	Val	Gly	Ser	Asp	Asn	Ser	Asp	
230															240	
ccc cag aag ata cgg agc ttg aag gtt tta cca ttc tta gac tct gag															825	
Pro	Gln	Lys	Ile	Arg	Ser	Leu	Lys	Val	Leu	Pro	Phe	Leu	Asp	Ser	Glu	
245															255	
tct ctg aac aaa ttg gtc cga gcc aca ttt gag ttg acg cgt gaa gat															873	
Ser	Leu	Asn	Lys	Leu	Val	Arg	Ala	Thr	Phe	Glu	Leu	Thr	Arg	Glu	Asp	
260															270	
att acg aaa ctc agg cac aag gtt aat cat cag tta tca aaa tca tca															921	
Ile	Thr	Lys	Leu	Arg	His	Lys	Val	Asn	His	Gln	Leu	Ser	Lys	Ser	Ser	
275															290	
aaa tca aag caa gtt cgt tta tca act ttt gtg ctt aca tta gct tat															969	
Lys	Ser	Lys	Gln	Val	Arg	Leu	Ser	Thr	Phe	Val	Leu	Thr	Leu	Ala	Tyr	

295	300	305	
gtg ttt gtt tgc atg gct aaa gct aaa tta gcc aaa gcc aaa act gaa Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys Thr Glu 310	315	320	1017
gct gaa gct gca gca ggt aat gat gaa att aaa aat att att gtg gga Ala Glu Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile Val Gly 325	330	335	1065
ttc act gcg gat tat agg agc cgt ttg gat cct cca att cca ctt aat Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro Leu Asn 340	345	350	1113
tat ttt ggt aac tgc aat ggg aga cat tgt gag act gca aaa gca agt Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys Ala Ser 355	360	365	1161
gat ttc gtt caa gaa aat ggg gtt gct ttt gtt gca gag atg tta agt Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met Leu Ser 375	380	385	1209
gat atg gtc aaa ggg atc gat gcg gat gcc att gaa gcc aat gat gat Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn Asp Asp 390	395	400	1257
aag gtt tca gaa ata ttg gaa att ctg aaa gaa gga gca atg att ttt Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met Ile Phe 405	410	415	1305
tct gtg gct ggc tcg acc caa ttt gat gtt tac ggg tcg gat ttc ggg Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp Phe Gly 420	425	430	1353
tgg ggg agg ccc aag aag gtg gag att gtg tca ata gat agg aca caa Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg Thr Gln 435	440	445	1401
gcc atc tct ttg gca gag aga aga gat gga gga ggc ggc gtt gag gtt Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Val Glu Val 455	460	465	1449
gga gtt gtt tta gag aag caa caa atg gag gtt ttt gaa tct gta ttt Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser Val Phe 470	475	480	1497
gct gat gga ctg aaa aat gat ctt gtt taattaatga tgtatcatct Ala Asp Gly Leu Lys Asn Asp Leu Val 485	490		1544
aaatttctca atatattattt ggtcatattc aaaagaaata aattattgcg gatttttgtg			1604
accaccaaat aaaatactct ttttgaaaa aaaaaaaaaa aaaa			1648
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<213> Citrus limon			

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<220>
<223> Lemon acyl transferase

<400> 18
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Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr
1 5 10 15

cct tct gag cca acc cca tct acg gtt ttg tct ctc tca gct ctt gat 96
Pro Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp
20 25 30

tct cag ctt ttc ttg cgt ttc act att gag tat ctc ttg gtc tat aga 144
Ser Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg
35 40 45

cct cgc cct ggt ttg gac cca ctt gct acc gtg gct cgt gtc aag tcc 192
Pro Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser
50 55 60

gca ctc gcc aaa gcc ttg gtt cct tac tat ccc ctc gcg ggt cgg gtc 240
Ala Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val
65 70 75

aga gct aaa caa gac ggg tcg ggc tta ttg gaa gtc gtg tgt cta ggc 288
Arg Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly
80 85 90 95
caa ggc gct gtg ttc atc gaa gcc gtc gac cgt gaa agt acg atc acc 336
Gln Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr
100 105 110

gat ttt gag agt gct ccc agg tat gtt act cag tgg agg aaa ctg ctg 384
Asp Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu
115 120 125

tcg tta tac gtg gcg gat gtt ctc aaa ggg gcc cca cct ctt gtc gtt 432
Ser Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val
130 135 140

cag ctg act tgg ctt aga gat gga gcc gca gcg ctc ggt att ggc ttt 480
Gln Leu Thr Trp Leu Arg Asp Gly Ala Ala Leu Gly Ile Gly Phe
145 150 155

aac cat tgt gtt tgc gat ggt atc ggc agc gcc gag ttc ctc aac ttg 528
Asn His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu
160 165 170 175

ttt act gag tta tgt acg agc cgt cat aac gaa ctg ggt ggt ggc cat 576
Phe Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly His
180 185 190

tct ctg ccg aaa ccc gtt tgg gat cgc cac cta atg aac tcc tcc tca		624	
Ser Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser			
195	200	205	
tca cgt caa cag cat gca gat aca cgt gcc agc tca gtg agt cac ctg		672	
Ser Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu			
210	215	220	
gaa ttc aac aga gtg gct gat ctt tgt ggt ttt gtt tct cgt ttt tcc		720	
Glu Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser			
225	230	235	
aac gaa agg ctt gtt ccc act tca ata acg ttc gat aaa cga cgc tta		768	
Asn Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu			
240	245	250	255
aac gag ctg cgg aag ctg gct ctg tcc acg agt cga ccc agt gag ctg		816	
Asn Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu			
260	265	270	
gct tac acg tca ttt gaa gtt ctt tca gct cat gtg tgg aga agc tgg		864	
Ala Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp			
275	280	285	
gct agg tcg ttg aat ctt ccg tcg aat caa atc ttg aag ctt cta ttt		912	
Ala Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe			
290	295	300	
agc atc aat gta cgt aac cgt gtc aag ccg agt ctc ccc agt ggc tat		960	
Ser Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr			
305	310	315	
tat ggc gat gca ttt gta tta ggc tgt gct caa acg agg gtt aaa gat		1008	
Tyr Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp			
320	325	330	335
ttg aca gag aag gac tta ggg cat gca gca atg ttg gtt aaa aag gcg		1056	
Leu Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala			
340	345	350	
aaa gag aga gtt gat agt gag tat gtg aag tcg gtc atc gac tca gtg		1104	
Lys Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val			
355	360	365	
agt cac acg aga gcg tgt ccc gac tca gtc ggg gtg ttg ata gtg tcg		1152	
Ser His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser			
370	375	380	
cag tgg tca agg cta ggg tta gag aga gtt gac ttt ggg atg ggg agg		1200	
Gln Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg			
385	390	395	
ccg act caa gtg ggt ccc att tgc tgc gac agg tat tgc ctg ttt cta		1248	
Pro Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu			
400	405	410	415
ccg gtt ttc aat cag acg gac gct gtt aag gtg atg gtg gcg gtc ccc		1296	

Pro Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro
 420 425 430
 aca agt gca gtt gac aag tat gag cat ctc gcg aag ggc tta tgc tgg 1344
 Thr Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
 435 440 445
 tgaggaccac accgcatgat gacccacca tgtaatacgt tgacttataa actcagttg 1404
 acttttaact ttttaacaa gtgatggaat ttcagtgatt gactcatcac tttgatcctg 1464
 atccaataaa taattgaatt gagttcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1520
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 <211> 455
 <212> PRT
 <213> Fragaria vesca
 <220>
 <223> Strawberry vesca alcohol acyl transferase
 <400> 19
 Met Glu Lys Ile Glu Val Ser Ile Ile Ser Lys His Thr Ile Lys Pro
 1 5 10 15
 Ser Thr Ser Ser Pro Leu Gln Pro Tyr Lys Leu Thr Leu Leu Asp
 20 25 30
 Gln Leu Thr Pro Pro Ser Tyr Val Pro Met Val Phe Phe Tyr Pro Ile
 35 40 45
 Thr Gly Pro Ala Val Phe Asn Leu Gln Thr Leu Ala Asp Leu Arg His
 50 55 60
 Ala Leu Ser Glu Thr Leu Thr Leu Tyr Tyr Pro Leu Ser Gly Arg Val
 65 70 75 80
 Lys Asn Asn Leu Tyr Ile Asp Asp Phe Glu Glu Gly Val Pro Tyr Leu
 85 90 95
 Glu Ala Arg Val Asn Cys Asp Met Asn Asp Phe Leu Arg Leu Pro Lys
 100 105 110
 Ile Glu Cys Leu Asn Glu Phe Val Pro Ile Lys Pro Phe Ser Met Glu
 115 120 125
 Ala Ile Ser Asp Glu Arg Tyr Pro Leu Leu Gly Val Gln Val Asn Ile
 130 135 140
 Phe Asn Ser Gly Ile Ala Ile Gly Val Ser Val Ser His Lys Leu Ile
 145 150 155 160
 Asp Gly Arg Thr Ser Asp Cys Phe Leu Lys Ser Trp Cys Ala Val Phe
 165 170 175
 Arg Gly Ser Arg Asp Lys Ile Ile His Pro Asn Leu Ser Gln Ala Ala
 180 185 190

Leu Leu Phe Pro Pro Arg Asp Asp Leu Pro Glu Lys Tyr Ala Arg Gln
 195 200 205
 Met Glu Gly Leu Trp Phe Val Gly Lys Lys Val Ala Thr Arg Arg Phe
 210 215 220
 Val Phe Gly Ala Lys Ala Ile Ser Val Ile Gln Asp Glu Ala Lys Ser
 225 230 235 240
 Glu Ser Val Pro Lys Pro Ser Arg Val Gln Ala Val Thr Ser Phe Leu
 245 250 255
 Trp Lys His Leu Ile Ala Thr Ser Arg Ala Leu Thr Ser Gly Thr Thr
 260 265 270
 Ser Thr Arg Leu Ser Ile Ala Thr Gln Val Val Asn Ile Arg Ser Arg
 275 280 285
 Arg Asn Met Glu Thr Val Trp Asp Asn Ala Ile Gly Asn Leu Ile Trp
 290 295 300
 Phe Ala Pro Ala Ile Leu Glu Leu Ser His Thr Thr Leu Glu Ile Ser
 305 310 315 320
 Asp Leu Lys Leu Cys Asp Leu Val Asn Leu Leu Asn Gly Ser Val Lys
 325 330 335
 Gln Cys Asn Gly Asp Tyr Phe Glu Thr Phe Met Gly Lys Glu Gly Tyr
 340 345 350
 Gly Ser Met Cys Glu Tyr Leu Asp Phe Gln Arg Thr Met Ser Ser Met
 355 360 365
 Glu Pro Ala Pro Glu Ile Tyr Leu Phe Thr Ser Trp Thr Asn Phe Phe
 370 375 380
 Asn Gln Leu Asp Phe Gly Trp Gly Arg Thr Ser Trp Ile Gly Val Ala
 385 390 395 400
 Gly Lys Ile Glu Ser Ala Phe Cys Asn Leu Thr Thr Leu Val Pro Thr
 405 410 415
 Pro Cys Asp Thr Gly Ile Glu Ala Trp Val Asn Leu Glu Glu Lys
 420 425 430
 Met Ala Met Leu Glu Gln Asp Pro Gln Phe Leu Ala Leu Ala Ser Pro
 435 440 445
 Lys Thr Leu Ile Ser Arg Tyr
 450 455
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 <211> 419
 <212> PRT
 <213> Musa sp.

<220>

<223> Banana alcohol acyl transferase

<400> 20

Met Ser Phe Ala Val Thr Arg Thr Ser Arg Ser Leu Val Thr Pro Cys
1 5 10 15

Gly Val Thr Pro Thr Gly Ser Leu Gly Leu Ser Ala Ile Asp Arg Val
20 25 30

Pro Gly Leu Arg His Met Val Arg Ser Leu His Val Phe Arg Gln Gly
35 40 45

Arg Glu Pro Ala Arg Ile Ile Arg Glu Ala Leu Ser Lys Ala Leu Val
50 55 60

Lys Tyr Tyr Pro Phe Ala Gly Arg Phe Val Asp Asp Pro Glu Gly Gly
65 70 75 80

Gly Glu Val Arg Val Ala Cys Thr Gly Glu Gly Ala Trp Phe Val Glu
85 90 95

Ala Lys Ala Asp Cys Ser Leu Glu Asp Val Lys Tyr Leu Asp Leu Pro
100 105 110

Leu Met Ile Pro Glu Asp Ala Leu Leu Pro Lys Pro Cys Pro Gly Leu
115 120 125

Asn Pro Leu Asp Leu Pro Leu Met Leu Gln Val Thr Glu Phe Val Gly
130 135 140

Gly Gly Phe Val Val Gly Leu Ile Ser Val His Thr Ile Ala Asp Gly
145 150 155 160

Leu Gly Val Val Gln Phe Ile Asn Ala Val Ala Glu Ile Ala Arg Gly
165 170 175

Leu Pro Lys Pro Thr Val Glu Pro Ala Trp Ser Arg Glu Val Ile Pro
180 185 190

Asn Pro Pro Lys Leu Pro Pro Gly Gly Pro Pro Val Phe Pro Ser Phe
195 200 205

Lys Leu Leu His Ala Thr Val Asp Leu Ser Pro Asp His Ile Asp His
210 215 220

Val Lys Ser Arg His Leu Glu Leu Thr Gly Gln Arg Cys Ser Thr Phe
225 230 235 240

Asp Val Ala Ile Ala Asn Leu Trp Gln Ser Arg Thr Arg Ala Ile Asn
245 250 255

Leu Asp Pro Gly Val Asp Val His Val Cys Phe Phe Ala Asn Thr Arg
260 265 270

His Leu Leu Arg Gln Val Val Leu Leu Pro Pro Glu Asp Gly Tyr Tyr
275 280 285

Gly Asn Cys Phe Tyr Pro Val Thr Ala Thr Ala Pro Ser Gly Arg Ile
 290 295 300
 Ala Ser Ala Glu Leu Ile Asp Val Val Ser Ile Ile Arg Asp Ala Lys
 305 310 315 320
 Ser Arg Leu Pro Gly Glu Phe Ala Lys Trp Ala Ala Gly Asp Phe Lys
 325 330 335
 Asp Asp Pro Tyr Glu Leu Ser Phe Thr Tyr Asn Ser Leu Phe Val Ser
 340 345 350
 Asp Trp Thr Arg Leu Gly Phe Leu Asp Val Asp Tyr Gly Trp Gly Lys
 355 360 365
 Pro Leu His Val Ile Pro Phe Ala Tyr Leu Asp Ile Met Ala Val Gly
 370 375 380
 Ile Ile Gly Ala Pro Pro Ala Pro Gln Lys Gly Thr Arg Val Met Ala
 385 390 395 400
 Gln Cys Val Glu Lys Glu His Met Gln Ala Phe Leu Glu Glu Met Lys
 405 410 415
 Gly Phe Ala

<210> 21
 <211> 454
 <212> PRT
 <213> Malus sp.

<220>
 <223> Apple alcohol acyl transferase

<400> 21
 Met Ser Phe Ser Val Leu Gln Val Lys Arg Leu Gln Pro Glu Leu Ile
 1 5 10 15

Thr Pro Ala Lys Ser Thr Pro Gln Glu Thr Lys Phe Leu Ser Asp Ile
 20 25 30
 Asp Asp Gln Glu Ser Leu Arg Val Gln Ile Pro Ile Ile Met Cys Tyr
 35 40 45

Lys Asp Asn Pro Ser Leu Asn Lys Asn Arg Asn Pro Val Lys Ala Ile
 50 55 60

Arg Glu Ala Leu Ser Arg Ala Leu Val Tyr Tyr Tyr Pro Leu Ala Gly
 65 70 75 80

Arg Leu Arg Glu Gly Pro Asn Arg Lys Leu Val Val Asp Cys Asn Gly
 85 90 95

Glu Gly Ile Leu Phe Val Glu Ala Ser Ala Asp Val Thr Leu Glu Gln
 100 105 110

Leu Gly Asp Lys Ile Leu Pro Pro Cys Pro Leu Leu Glu Glu Phe Leu

115	120	125	
Tyr Asn Phe Pro Gly Ser Asp Gly Ile Ile Asp Cys Pro Leu Leu Leu			
130	135	140	
Ile Gln Val Thr Cys Leu Thr Cys Gly Gly Phe Ile Leu Ala Leu Arg			
145	150	155	160
Leu Asn His Thr Met Cys Asp Ala Ala Gly Leu Leu Leu Phe Leu Thr			
165	170	175	
Ala Ile Ala Glu Met Ala Arg Gly Ala His Ala Pro Ser Ile Leu Pro			
180	185	190	
Val Trp Glu Arg Glu Leu Leu Phe Ala Arg Asp Pro Pro Arg Ile Thr			
195	200	205	
Cys Ala Arg His Glu Tyr Glu Asp Val Ile Gly His Ser Asp Gly Ser			
210	215	220	
Tyr Ala Ser Ser Asn Gln Ser Asn Met Val Gln Arg Ser Phe Tyr Phe			
225	230	235	240
Gly Ala Lys Glu Met Arg Val Leu Arg Lys Gln Ile Pro Pro His Leu			
245	250	255	
Ile Ser Thr Cys Ser Thr Phe Asp Leu Ile Thr Ala Cys Leu Trp Lys			
260	265	270	
Cys Arg Thr Leu Ala Leu Asn Ile Asn Pro Lys Glu Ala Val Arg Val			
275	280	285	
Ser Cys Ile Val Asn Ala Arg Gly Lys His Asn Asn Val Arg Leu Pro			
290	295	300	
Leu Gly Tyr Tyr Gly Asn Ala Phe Ala Phe Pro Ala Ala Ile Ser Lys			
305	310	315	320
Ala Glu Pro Leu Cys Lys Asn Pro Leu Gly Tyr Ala Leu Glu Leu Val			
325	330	335	
Lys Lys Ala Lys Ala Thr Met Asn Glu Glu Tyr Leu Arg Ser Val Ala			
340	345	350	
Asp Leu Leu Val Leu Arg Gly Arg Pro Gln Tyr Ser Ser Thr Gly Ser			
355	360	365	
Tyr Leu Ile Val Ser Asp Asn Thr Arg Val Gly Phe Gly Asp Val Asn			
370	375	380	
Phe Gly Trp Gly Gln Pro Val Phe Ala Gly Pro Val Lys Ala Leu Asp			
385	390	395	400
Leu Ile Ser Phe Tyr Val Gln His Lys Asn Asn Thr Glu Asp Gly Ile			
405	410	415	
Leu Val Pro Met Cys Leu Pro Ser Ser Ala Met Glu Arg Phe Gln Gln			
420	425	430	

Glu Leu Glu Arg Ile Thr Gln Glu Pro Lys Glu Asp Ile Cys Asn Asn
 435 440 445
 Leu Arg Ser Thr Ser Gln
 450
 <210> 22
 <211> 431
 <212> PRT
 <213> Mangifera indica
 <220>
 <223> Mango alcohol acyl transferase
 <400> 22
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 Thr Pro Arg Ile Ser Leu Trp Asn Ser Asn Ala Asp Leu Val Val Pro
 20 25 30
 Arg Phe His Thr Pro Ser Val Tyr Phe Tyr Arg Pro Thr Gly Ala Ile
 35 40 45
 Asn Phe Phe Asp Gly Lys Leu Leu Lys Glu Ala Leu Gly Lys Ala Leu
 50 55 60
 Val Pro Phe Tyr Pro Met Ala Gly Arg Leu Lys Arg Asp Glu Asp Gly
 65 70 75 80
 Arg Ile Glu Ile Asp Cys Asn Ala Glu Gly Val Leu Phe Val Glu Ala
 85 90 95
 Glu Thr Pro Ser Val Ile Asp Asp Phe Gly Asp Phe Ala Pro Thr Leu
 100 105 110
 Glu Leu Lys Gln Leu Ile Pro Thr Val Asp Tyr Ser Gly Gly Ile Ser
 115 120 125
 Thr Tyr Pro Leu Leu Ala Leu Gln Val Thr His Phe Lys Cys Gly Gly
 130 135 140
 Val Ser Leu Gly Val Gly Met Gln His His Ala Ala Asp Gly Phe Ser
 145 150 155 160
 Gly Leu His Phe Val Asn Thr Trp Ser Asp Ile Ala Arg Gly Leu Asp
 165 170 175
 Val Asn Ile Thr Leu Phe Ile Asp Arg Thr Leu Leu Arg Ala Gln Asp
 180 185 190
 Pro Pro Gln Pro Thr Phe Pro His Thr Trp Asn Thr Arg Pro Pro Pro
 195 200 205
 Ser Leu Lys Thr Pro Pro Pro Ala Val Ser Glu Pro Thr Ala Val Ser
 210 215 220

Ile Phe Lys Leu Thr Arg Asp Gln Leu Asn Ile Leu Lys Ala Lys Ala
 225 230 235 240
 Lys Glu Asp Gly Asn Thr Ile Asn Tyr Ser Ser Tyr Glu Met Leu Ala
 245 250 255
 Gly His Val Trp Arg Ser Ala Cys Lys Ala Arg Gly Leu Ser Asp Asp
 260 265 270
 Gln Glu Thr Lys Leu Tyr Ile Ala Thr Asp Gly Arg Ala Arg Leu Ile
 275 280 285
 Pro Pro Leu Pro Pro Gly Tyr Phe Gly Asn Val Ile Phe Thr Ala Thr
 290 295 300
 Pro Met Ala Val Ala Gly Asp Leu Gln Ser Lys Pro Ile Trp Tyr Ala
 305 310 315 320
 Ala Gly Gln Ile His Asp Ala Leu Val Arg Met Asp Asn Asp Tyr Leu
 325 330 335
 Arg Ser Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Ala Leu
 340 345 350
 Val Arg Gly Ala His Thr Phe Arg Cys Pro Asn Leu Gly Ile Thr Ser
 355 360 365
 Trp Val Arg Leu Pro Ile His Asp Ala Asp Phe Gly Trp Gly Pro Pro
 370 375 380
 Thr Phe Met Gly Pro Gly Gly Ile Ala Tyr Glu Gly Leu Ser Phe Val
 385 390 395 400
 Leu Pro Ser Pro Thr Asn Asp Gly Ser Leu Ser Val Ala Ile Ser Leu
 405 410 415
 Gln Ser Glu His Met Lys Leu Phe Gln Lys Phe Phe Tyr Asp Ile
 420 425 430
 <210> 23
 <211> 426
 <212> PRT
 <213> Citrus limon
 <220>
 <223> Lemon acyl transferase
 <400> 23
 Met Asp Leu Gln Ile Thr Cys Thr Glu Ile Ile Lys Pro Ser Ser Pro
 1 5 10 15
 Thr Pro Gln His Gln Ser Thr Tyr Lys Leu Ser Ile Ile Asp Gln Leu
 20 25 30
 Thr Pro Asn Val Tyr Phe Ser Ile Ile Leu Tyr Ser Lys Ala Gly
 35 40 45

Glu Ser Thr Ala Lys Thr Ser Asp His Leu Lys Glu Ser Leu Ser Asn
 50 55 60

Thr Leu Thr His Tyr Tyr Pro Leu Ala Gly Gln Leu Lys Tyr Asp Gln
 65 70 75 80

Leu Ile Val Asp Cys Asn Asp Gln Gly Val Pro Phe Ile Glu Ala His
 85 90 95

Val Thr Asn Asp Met Arg Gln Leu Leu Lys Ile Pro Asn Ile Asp Val
 100 105 110

Leu Glu Gln Leu Leu Pro Phe Lys Pro His Glu Gly Phe Asp Ser Asp
 115 120 125

Arg Ser Asn Leu Thr Val Gln Val Asn Tyr Phe Gly Cys Glu Gly Met
 130 135 140

Ala Ile Gly Leu Cys Phe Arg His Lys Val Ile Asp Ala Thr Thr Ala
 145 150 155 160

Ala Phe Phe Val Lys Asn Trp Gly Val Ile Ala Arg Gly Ala Gly Glu
 165 170 175

Ile Lys Asp Val Ile Ile Asp His Ala Ser Leu Phe Pro Ala Arg Asp
 180 185 190

Leu Ser Cys Leu Thr Lys Ser Val Asp Glu Glu Phe Leu Lys Pro Glu
 195 200 205

Ser Glu Thr Lys Arg Phe Val Phe Asp Gly Ala Thr Ile Ala Ser Leu
 210 215 220

Gln Glu Thr Phe Ala Ser Phe Glu Arg Arg Pro Thr Arg Phe Glu Val
 225 230 235 240

Val Ser Ala Val Ile Leu Gly Ala Leu Ile Thr Ala Thr Arg Glu Ser
 245 250 255

Asp Asp Glu Ser Asn Val Pro Glu Arg Leu Asp Thr Ile Ile Ser Val
 260 265 270

Asn Leu Arg Gln Arg Met Asn Pro Pro Phe Pro Glu His Cys Met Gly
 275 280 285

Asn Ile Ile Ser Gly Gly Leu Val Tyr Trp Pro Leu Glu Lys Lys Val
 290 295 300

Asp Tyr Gly Cys Leu Ala Lys Glu Ile His Glu Ser Ile Lys Lys Val
 305 310 315 320

Asp Asp Gln Phe Ala Arg Lys Phe Tyr Gly Asp Ala Glu Phe Leu Asn
 325 330 335

Leu Pro Arg Leu Ala Gly Ala Glu Asp Val Lys Lys Arg Glu Phe Trp
 340 345 350

Val Thr Ser Trp Cys Lys Thr Pro Leu Tyr Glu Ala Asp Phe Gly Trp
 355 360 365
 Gly Asn Pro Lys Trp Ala Gly Asn Ser Met Arg Leu Asn Gln Ile Thr
 370 375 380
 Val Phe Phe Asp Ser Ser Asp Gly Glu Gly Val Glu Ala Trp Val Gly
 385 390 395 400
 Leu Pro Arg Lys Asp Met Ala Arg Phe Glu Lys Asp Ser Gly Ile Leu
 405 410 415
 Ala Tyr Thr Ser Pro Asn Pro Ser Ile Phe
 420 425
 <210> 24
 <211> 491
 <212> PRT
 <213> Citrus limon
 <220>
 <223> Lemon acyl transferase
 <400> 24
 Met Ala Ala Ile Glu Asn Arg Val Thr Leu Lys Lys His Glu Val Thr
 1 5 10 15
 Lys Val Thr Pro Phe Val Asn Pro Asn Ser Lys Thr Thr Ser Phe Thr
 20 25 30
 Leu Asp Leu Thr Tyr Phe Asp Phe Trp Phe Lys Asn Pro Pro Val
 35 40 45
 Glu Arg Leu Phe Phe Tyr Glu Met Thr Asp Leu Thr Trp Asp Leu Phe
 50 55 60
 Asn Ser Glu Ile Leu Pro Lys Leu Lys His Ser Leu Ser Phe Thr Leu
 65 70 75 80
 Leu His Tyr Leu Pro Leu Ala Gly His Ile Met Trp Pro Leu Asp Ala
 85 90 95
 Ala Lys Pro Ala Val Tyr Tyr Phe Pro Asp Gln Asn Asp Gly Val Ser
 100 105 110
 Phe Ala Val Ala Glu Trp Ser Ser Glu Cys His Ala Gly Phe His His
 115 120 125
 Leu Ser Gly Asn Gly Ile Arg Gln Ala Val Glu Phe His Pro Leu Val
 130 135 140
 Pro Gln Leu Ser Leu Thr Asp Asp Lys Ala Glu Val Ile Ala Ile Gln
 145 150 155 160
 Ile Thr Leu Phe Pro Asn Gln Gly Phe Ser Ile Gly Val Ser Ser His
 165 170 175

His Ala Ile Leu Asp Gly Lys Thr Ser Thr Leu Phe Leu Lys Ser Trp
 180 185 190

Ala Tyr Leu Cys Lys Gln Leu Gln Leu Cys His His Pro Cys Leu Ser
 195 200 205

Pro Glu Leu Thr Pro Leu Leu Asp Arg Thr Val Ile Lys Asp Pro Thr
 210 215 220

Gly Gln Asp Met Leu Gln Leu Asn Lys Trp Val Val Gly Ser Asp Asn
 225 230 235 240

Ser Asp Pro Gln Lys Ile Arg Ser Leu Lys Val Leu Pro Phe Leu Asp
 245 250 255

Ser Glu Ser Leu Asn Lys Leu Val Arg Ala Thr Phe Glu Leu Thr Arg
 260 265 270

Glu Asp Ile Thr Lys Leu Arg His Lys Val Asn His Gln Leu Ser Lys
 275 280 285

Ser Ser Lys Ser Lys Gln Val Arg Leu Ser Thr Phe Val Leu Thr Leu
 290 295 300

Ala Tyr Val Phe Val Cys Met Ala Lys Ala Lys Leu Ala Lys Ala Lys
 305 310 315 320

Thr Glu Ala Glu Ala Ala Gly Asn Asp Glu Ile Lys Asn Ile Ile
 325 330 335

Val Gly Phe Thr Ala Asp Tyr Arg Ser Arg Leu Asp Pro Pro Ile Pro
 340 345 350

Leu Asn Tyr Phe Gly Asn Cys Asn Gly Arg His Cys Glu Thr Ala Lys
 355 360 365

Ala Ser Asp Phe Val Gln Glu Asn Gly Val Ala Phe Val Ala Glu Met
 370 375 380

Leu Ser Asp Met Val Lys Gly Ile Asp Ala Asp Ala Ile Glu Ala Asn
 385 390 395 400

Asp Asp Lys Val Ser Glu Ile Leu Glu Ile Leu Lys Glu Gly Ala Met
 405 410 415

Ile Phe Ser Val Ala Gly Ser Thr Gln Phe Asp Val Tyr Gly Ser Asp
 420 425 430

Phe Gly Trp Gly Arg Pro Lys Lys Val Glu Ile Val Ser Ile Asp Arg
 435 440 445

Thr Gln Ala Ile Ser Leu Ala Glu Arg Arg Asp Gly Gly Gly Val
 450 455 460

Glu Val Gly Val Val Leu Glu Lys Gln Gln Met Glu Val Phe Glu Ser
 465 470 475 480

Val Phe Ala Asp Gly Leu Lys Asn Asp Leu Val
 485 490
 <210> 25
 <211> 447
 <212> PRT
 <213> Citrus limon
 <220>
 <223> Lemon acyl transferase
 <400> 25
 Met Ala Ala Ser Ser Leu His Gly Lys Glu Ala Thr Val Ile Tyr Pro
 1 5 10 15
 Ser Glu Pro Thr Pro Ser Thr Val Leu Ser Leu Ser Ala Leu Asp Ser
 20 25 30
 Gln Leu Phe Leu Arg Phe Thr Ile Glu Tyr Leu Leu Val Tyr Arg Pro
 35 40 45
 Arg Pro Gly Leu Asp Pro Leu Ala Thr Val Ala Arg Val Lys Ser Ala
 50 55 60
 Leu Ala Lys Ala Leu Val Pro Tyr Tyr Pro Leu Ala Gly Arg Val Arg
 65 70 75 80
 Ala Lys Gln Asp Gly Ser Gly Leu Leu Glu Val Val Cys Leu Gly Gln
 85 90 95
 Gly Ala Val Phe Ile Glu Ala Val Asp Arg Glu Ser Thr Ile Thr Asp
 100 105 110
 Phe Glu Ser Ala Pro Arg Tyr Val Thr Gln Trp Arg Lys Leu Leu Ser
 115 120 125
 Leu Tyr Val Ala Asp Val Leu Lys Gly Ala Pro Pro Leu Val Val Gln
 130 135 140
 Leu Thr Trp Leu Arg Asp Gly Ala Ala Ala Leu Gly Ile Gly Phe Asn
 145 150 155 160
 His Cys Val Cys Asp Gly Ile Gly Ser Ala Glu Phe Leu Asn Leu Phe
 165 170 175
 Thr Glu Leu Cys Thr Ser Arg His Asn Glu Leu Gly Gly His Ser
 180 185 190
 Leu Pro Lys Pro Val Trp Asp Arg His Leu Met Asn Ser Ser Ser Ser
 195 200 205
 Arg Gln Gln His Ala Asp Thr Arg Ala Ser Ser Val Ser His Leu Glu
 210 215 220
 Phe Asn Arg Val Ala Asp Leu Cys Gly Phe Val Ser Arg Phe Ser Asn
 225 230 235 240

Glu Arg Leu Val Pro Thr Ser Ile Thr Phe Asp Lys Arg Arg Leu Asn
 245 250 255
 Glu Leu Arg Lys Leu Ala Leu Ser Thr Ser Arg Pro Ser Glu Leu Ala
 260 265 270
 Tyr Thr Ser Phe Glu Val Leu Ser Ala His Val Trp Arg Ser Trp Ala
 275 280 285
 Arg Ser Leu Asn Leu Pro Ser Asn Gln Ile Leu Lys Leu Leu Phe Ser
 290 295 300
 Ile Asn Val Arg Asn Arg Val Lys Pro Ser Leu Pro Ser Gly Tyr Tyr
 305 310 315 320
 Gly Asp Ala Phe Val Leu Gly Cys Ala Gln Thr Arg Val Lys Asp Leu
 325 330 335
 Thr Glu Lys Asp Leu Gly His Ala Ala Met Leu Val Lys Lys Ala Lys
 340 345 350
 Glu Arg Val Asp Ser Glu Tyr Val Lys Ser Val Ile Asp Ser Val Ser
 355 360 365
 His Thr Arg Ala Cys Pro Asp Ser Val Gly Val Leu Ile Val Ser Gln
 370 375 380
 Trp Ser Arg Leu Gly Leu Glu Arg Val Asp Phe Gly Met Gly Arg Pro
 385 390 395 400
 Thr Gln Val Gly Pro Ile Cys Cys Asp Arg Tyr Cys Leu Phe Leu Pro
 405 410 415
 Val Phe Asn Gln Thr Asp Ala Val Lys Val Met Val Ala Val Pro Thr
 420 425 430
 Ser Ala Val Asp Lys Tyr Glu His Leu Ala Lys Gly Leu Cys Trp
 435 440 445
 <210> 26
 <211> 456
 <212> PRT
 <213> Cucumis melo
 <220>
 <223> Honey dew melon alcohol acyl transferase
 <400> 26
 Met Asp Phe Ser Phe His Val Arg Lys Cys Gln Pro Glu Leu Ile Ala
 1 5 10 15
 Pro Ala Asn Pro Thr Pro Tyr Glu Phe Lys Gln Leu Ser Asp Val Asp
 20 25 30
 Asp Gln Gln Ser Leu Arg Leu Gln Leu Pro Phe Val Asn Ile Tyr Pro
 35 40 45

His	Asn	Pro	Ser	Leu	Glu	Gly	Arg	Asp	Pro	Val	Lys	Val	Ile	Lys	Glu
50					55					60					
Ala	Ile	Gly	Lys	Ala	Leu	Val	Phe	Tyr	Tyr	Pro	Leu	Ala	Gly	Arg	Leu
65					70					75					80
Arg	Glu	Gly	Pro	Gly	Arg	Lys	Leu	Phe	Val	Glu	Cys	Thr	Gly	Glu	Gly
					85					90					95
Ile	Leu	Phe	Ile	Glu	Ala	Asp	Ala	Asp	Val	Ser	Leu	Glu	Glu	Phe	Trp
					100					105					110
Asp	Thr	Leu	Pro	Tyr	Ser	Leu	Ser	Ser	Met	Gln	Asn	Asn	Ile	Ile	His
					115					120					125
Asn	Ala	Leu	Asn	Ser	Asp	Glu	Val	Leu	Asn	Ser	Pro	Leu	Leu	Leu	Ile
					130					135					140
Gln	Val	Thr	Arg	Leu	Lys	Cys	Gly	Gly	Phe	Ile	Phe	Gly	Leu	Cys	Phe
					145					150					160
Asn	His	Thr	Met	Ala	Asp	Gly	Phe	Gly	Ile	Val	Gln	Phe	Met	Lys	Ala
					165					170					175
Thr	Ala	Glu	Ile	Ala	Arg	Gly	Ala	Phe	Ala	Pro	Ser	Ile	Leu	Pro	Val
					180					185					190
Trp	Gln	Arg	Ala	Leu	Leu	Thr	Ala	Arg	Asp	Pro	Pro	Arg	Ile	Thr	Phe
					195					200					205
Arg	His	Tyr	Glu	Tyr	Asp	Gln	Val	Val	Asp	Met	Lys	Ser	Gly	Leu	Ile
					210					215					220
Pro	Val	Asn	Ser	Lys	Ile	Asp	Gln	Leu	Phe	Phe	Phe	Ser	Gln	Leu	Gln
					225					230					240
Ile	Ser	Thr	Leu	Arg	Gln	Thr	Leu	Pro	Ala	His	Leu	His	Asp	Cys	Pro
					245					250					255
Ser	Phe	Glu	Val	Leu	Thr	Ala	Tyr	Val	Trp	Arg	Leu	Arg	Thr	Ile	Ala
					260					265					270
Leu	Gln	Phe	Lys	Pro	Glu	Glu	Glu	Val	Arg	Phe	Leu	Cys	Val	Met	Asn
					275					280					285
Leu	Arg	Ser	Lys	Ile	Asp	Ile	Pro	Leu	Gly	Tyr	Tyr	Gly	Asn	Ala	Val
					290					295					300
Val	Val	Pro	Ala	Val	Ile	Thr	Thr	Ala	Ala	Lys	Leu	Cys	Gly	Asn	Pro
					305					310					320
Leu	Gly	Tyr	Ala	Val	Asp	Leu	Ile	Arg	Lys	Ala	Lys	Ala	Lys	Ala	Thr
					325					330					335
Met	Glu	Tyr	Ile	Lys	Ser	Thr	Val	Asp	Leu	Met	Val	Ile	Lys	Gly	Arg
					340					345					350

Pro Tyr Phe Thr Val Val Gly Ser Phe Met Met Ser Asp Leu Thr Arg
355 360 365

Ile Gly Val Glu Asn Val Asp Phe Gly Trp Gly Lys Ala Ile Phe Gly
370 375 380

Gly Pro Thr Thr Thr Gly Ala Arg Ile Thr Arg Gly Leu Val Ser Phe
385 390 395 400

Cys Val Pro Phe Met Asn Arg Asn Gly Glu Lys Gly Thr Ala Leu Ser
405 410 415

Leu Cys Leu Pro Pro Pro Ala Met Glu Arg Phe Arg Ala Asn Val His
420 425 430

Ala Ser Leu Gln Val Lys Gln Val Val Asp Ala Val Asp Ser His Met
435 440 445

Gln Thr Ile Gln Ser Ala Ser Lys
450 455

<210> 27

<211> 397

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry aminotransferase

<400> 27

Met Ala Lys Leu Gln Ala Gly Tyr Leu Phe Pro Glu Ile Ala Arg Arg
1 5 10 15

Arg Asn Ala His Leu Gln Lys His Pro Asp Ala Lys Ile Ile Pro Leu
20 25 30

Gly Ile Gly Asp Thr Thr Glu Pro Ile Pro Glu Tyr Ile Thr Ser Ala
35 40 45

Met Ala Lys Arg Ala Leu Ala Met Ser Thr Leu Glu Gly Tyr Ser Gly
50 55 60

Tyr Gly Pro Glu Gln Gly Glu Lys Pro Leu Arg Val Ala Ile Ala Lys
65 70 75 80

Thr Phe Tyr Gly Asp Leu Gly Ile Glu Glu Asp Asp Ile Phe Val Ser
85 90 95

Asp Gly Ala Lys Cys Asp Ile Ser Arg Leu Gln Val Leu Phe Gly Ala
100 105 110

Asp Lys Thr Ile Ala Val Gln Asp Pro Ser Tyr Pro Ala Tyr Val Asp
115 120 125

Ser Ser Val Ile Met Gly Gln Thr Gly Gln Tyr Gln Lys Ser Val Gln
130 135 140

Lys Phe Gly Asn Ile Glu Tyr Met Arg Cys Thr Pro Asp Asn Gly Phe
 145 150 155 160
 Phe Pro Asp Leu Ser Ser Thr Lys Arg Thr Asp Ile Ile Phe Phe Cys
 165 170 175
 Ser Pro Asn Asn Pro Thr Gly Ser Ala Ala Thr Arg Glu Gln Leu Thr
 180 185 190
 Gln Leu Val Lys Phe Ala Lys Asp Asn Gly Ser Ile Ile Val Tyr Asp
 195 200 205
 Ser Ala Tyr Ala Met Tyr Met Ser Asp Asp Asn Pro Arg Ser Ile Phe
 210 215 220
 Glu Ile Pro Gly Ala Lys Asp Val Ala Leu Glu Thr Ser Ser Phe Ser
 225 230 235 240
 Lys Tyr Ala Gly Phe Thr Gly Val Arg Leu Gly Trp Thr Val Val Pro
 245 250 255
 Lys Gln Leu Gln Tyr Ser Asp Gly Phe Gln Val Ala Lys Asp Phe Asn
 260 265 270
 Arg Ile Val Cys Thr Cys Phe Asn Gly Ala Ser Thr Ile Ile Gln Ala
 275 280 285
 Gly Gly Leu Ala Cys Leu Gln Pro Lys Gly Val Lys Ala Met His Gly
 290 295 300
 Val Ile Asn Phe Tyr Lys Glu Asn Thr Lys Ile Ile Met Glu Thr Phe
 305 310 315 320
 Asn Ser Leu Gly Phe Asn Val Tyr Gly Gly Thr Asn Ala Pro Tyr Val
 325 330 335
 Trp Val His Phe Pro Gly Gln Ser Ser Trp Asp Val Phe Ala Glu Ile
 340 345 350
 Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly Pro
 355 360 365
 Gly Gly Glu Gly Phe Ile Arg Val Ser Ala Phe Gly His Arg Lys Asn
 370 375 380
 Ile Leu Glu Ala Cys Lys Arg Phe Lys Gln Leu Tyr Lys
 385 390 395
 <210> 28
 <211> 458
 <212> PRT
 <213> Fragaria x ananassa
 <220>
 <223> Strawberry thiolase
 <400> 28

Met Glu Lys Ala Ile Asn Arg Gln Lys Val Leu Leu Asp His Leu Arg
 1 5 10 15

Pro Ser Ser Ser Ser Asp Asp Ser Ser Leu Ser Ala Ser Val Cys Ala
 20 25 30

Ala Gly Asp Ser Ala Ala Tyr Ala Arg Asn His Val Phe Gly Asp Asp
 35 40 45

Val Val Ile Val Ala Ala Phe Arg Thr Pro Leu Cys Lys Ala Lys Arg
 50 55 60

Gly Gly Phe Lys Tyr Thr Tyr Ala Asp Asp Leu Leu Ala Pro Val Leu
 65 70 75 80

Lys Ala Val Val Glu Lys Thr Asn Leu Asn Pro Lys Glu Val Gly Asp
 85 90 95

Ile Val Val Gly Thr Val Leu Ala Pro Gly Ser Gln Arg Ala Ser Glu
 100 105 110

Cys Arg Met Ala Ala Phe Tyr Ala Gly Phe Pro Glu Thr Val Pro Val
 115 120 125

Arg Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Asp
 130 135 140

Val Ala Ala Ala Ile Arg Ala Gly Phe Tyr Asp Ile Gly Ile Gly Ala
 145 150 155 160

Gly Leu Glu Ser Met Thr Ala Asn Pro Met Ala Trp Glu Gly Asp Val
 165 170 175

Asn Pro Lys Val Lys Ile Phe Glu Gln Ala Gln Asn Cys Leu Leu Pro
 180 185 190

Met Gly Val Thr Ser Glu Asn Val Ala His Arg Phe Gly Val Ser Arg
 195 200 205

Gln Glu Gln Asp Gln Ala Ala Val Asp Ser His Arg Lys Ala Ala Ala
 210 215 220

Ala Ala Ala Ala Gly Arg Phe Lys Asp Glu Ile Ile Pro Val Ala Thr
 225 230 235 240

Lys Ile Val Asp Pro Lys Ser Gly Asp Glu Lys Pro Val Thr Ile Ser
 245 250 255

Val Asp Asp Gly Ile Arg Asn Thr Thr Leu Ala Asp Leu Ala Lys Leu
 260 265 270

Lys Pro Val Phe Lys Lys Asp Gly Thr Thr Thr Ala Gly Asn Ser Ser
 275 280 285

Gln Val Ser Asp Gly Ala Gly Ala Val Leu Leu Met Lys Arg Ser Val
 290 295 300

Ala Asp Gln Lys Gly Leu Pro Ile Leu Gly Val Phe Arg Asn Phe Val
 305 310 315 320

Ala Val Gly Val Asp Pro Ala Ile Met Gly Val Gly Pro Ala Ala Ala
 325 330 335

Ile Pro Val Ala Val Lys Ala Ala Gly Leu Glu Leu Asp Asp Ile Asp
 340 345 350

Leu Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Phe Val Tyr Cys Arg
 355 360 365

Asn Lys Leu Gly Leu Asp Pro Glu Lys Ile Asn Val Asn Gly Gly Ala
 370 375 380

Met Ala Ile Gly His Pro Leu Gly Ala Thr Gly Ala Arg Cys Val Ala
 385 390 395 400

Thr Leu Leu His Glu Met Lys Arg Arg Gly Lys Asp Cys Arg Tyr Gly
 405 410 415

Val Ile Ser Met Cys Ile Gly Thr Gly Met Gly Ala Ala Val Phe
 420 425 430

Glu Arg Gly Asp Arg Thr Asp Glu Leu Cys Asn Ala Arg Lys Val Glu
 435 440 445

Ser Leu Asn Phe Leu Ser Lys Asp Val Arg
 450 455

<210> 29
 <211> 605
 <212> PRT
 <213> Fragaria x ananassa

<220>
 <223> Strawberry pyruvate decarboxylase

<400> 29
 Met Asp Thr Lys Ile Gly Ser Ile Asp Val Cys Lys Thr Glu Asn His
 1 5 10 15

Asp Val Gly Cys Leu Pro Asn Ser Ala Thr Ser Thr Val Gln Asn Ser
 20 25 30

Val Pro Ser Thr Ser Leu Ser Ser Ala Asp Ala Thr Leu Gly Arg His
 35 40 45

Leu Ala Arg Arg Leu Val Gln Ile Gly Val Thr Asp Val Phe Thr Val
 50 55 60

Pro Gly Asp Phe Asn Leu Thr Leu Leu Asp His Leu Ile Ala Glu Pro
 65 70 75 80

Gly Leu Thr Asn Ile Gly Cys Cys Asn Glu Leu Asn Ala Gly Tyr Ala
 85 90 95

Ala Asp Gly Tyr Ala Arg Ser Arg Gly Val Gly Ala Cys Val Val Thr
100 105 110

Phe Thr Val Gly Gly Leu Ser Val Leu Asn Ala Ile Ala Gly Ala Tyr
115 120 125

Ser Glu Asn Leu Pro Val Ile Cys Ile Val Gly Gly Pro Asn Ser Asn
130 135 140

Asp Tyr Gly Thr Asn Arg Ile Leu His His Thr Ile Gly Leu Pro Asp
145 150 155 160

Phe Ser Gln Glu Leu Arg Cys Phe Gln Thr Val Thr Cys Phe Gln Ala
165 170 175

Val Val Asn Asn Leu Glu Asp Ala His Glu Met Ile Asp Thr Ala Ile
180 185 190

Ser Thr Ala Leu Lys Glu Ser Lys Pro Val Tyr Ile Ser Ile Gly Cys
195 200 205

Asn Leu Ala Gly Ile Pro His Pro Thr Phe Ser Arg Glu Pro Val Pro
210 215 220

Phe Ser Leu Ser Pro Lys Leu Ser Asn Lys Trp Gly Leu Glu Ala Ala
225 230 235 240

Val Glu Ala Ala Ala Glu Phe Leu Asn Lys Ala Val Lys Pro Val Met
245 250 255

Val Gly Gly Pro Lys Leu Arg Ser Ala His Ala Gly Asp Ala Phe Val
260 265 270

Glu Leu Ala Asp Ala Ser Gly Phe Ala Leu Ala Val Met Pro Ser Ala
275 280 285

Lys Gly Gln Val Pro Glu His His Pro His Phe Ile Gly Thr Tyr Trp
290 295 300

Gly Ala Val Ser Thr Ala Phe Cys Ala Glu Ile Val Glu Ser Ala Asp
305 310 315 320

Ala Tyr Leu Phe Ala Gly Pro Ile Phe Asn Asp Tyr Ser Ser Val Gly
325 330 335

Tyr Ser Leu Leu Leu Lys Lys Glu Lys Ala Ile Ile Val Gln Pro Asp
340 345 350

Arg Val Thr Ile Gly Asn Gly Pro Thr Phe Gly Cys Val Leu Met Lys
355 360 365

Asp Phe Leu Leu Gly Leu Ala Lys Lys Leu Lys His Asn Asn Thr Ala
370 375 380

His Glu Asn Tyr Arg Arg Ile Phe Val Pro Asp Gly His Pro Leu Lys
385 390 395 400

Ala Ala Pro Lys Glu Pro Leu Arg Val Asn Val Leu Phe Lys His Ile
 405 410 415

 Gln Asn Met Leu Ser Ala Glu Thr Ala Val Ile Ala Glu Thr Gly Asp
 420 425 430

 Ser Trp Phe Asn Cys Gln Lys Leu Lys Leu Pro Pro Gly Cys Gly Tyr
 435 440 445

 Glu Phe Gln Met Gln Tyr Gly Ser Ile Gly Trp Ser Val Gly Ala Thr
 450 455 460

 Leu Gly Tyr Ala Gln Ala Val Pro Glu Lys Arg Val Ile Ser Phe Ile
 465 470 475 480

 Gly Asp Gly Ser Phe Gln Val Thr Ala Gln Asp Val Ser Thr Met Ile
 485 490 495

 Arg Asn Gly Gln Arg Thr Ile Ile Phe Leu Ile Asn Asn Gly Gly Tyr
 500 505 510

 Thr Ile Glu Val Glu Ile His Asp Gly Pro Tyr Asn Val Ile Lys Asn
 515 520 525
 Trp Asn Tyr Thr Gly Leu Val Asp Ala Ile His Asn Gly Glu Gly Lys
 530 535 540

 Cys Trp Thr Thr Lys Val Arg Cys Glu Glu Glu Leu Ile Glu Ala Ile
 545 550 555 560

 Glu Thr Ala Asn Gly Pro Lys Lys Asp Ser Phe Cys Phe Ile Glu Val
 565 570 575

 Ile Val His Lys Asp Asp Thr Ser Lys Glu Leu Leu Glu Trp Gly Ser
 580 585 590

 Arg Val Ser Ala Ala Asn Ser Arg Pro Pro Asn Pro Gln
 595 600 605

<210> 30
 <211> 333
 <212> PRT
 <213> Fragaria x ananassa

<220>
 <223> Strawberry alcohol dehydrogenase

 <400> 30
 Met Val Met Ser Ile Glu Gln Glu His Pro Lys Lys Ala Ser Gly Trp
 1 5 10 15

Ala Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Ser Phe Ser Arg
 20 25 30

Arg Glu Thr Gly Glu Lys Asp Val Thr Phe Lys Val Met Tyr Cys Gly
 35 40 45
 Ile Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser
 50 55 60
 Thr Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu
 65 70 75 80
 Val Gly Ser Asn Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val
 85 90 95
 Gly Cys Ile Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His
 100 105 110
 Leu Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr
 115 120 125
 Tyr Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala
 130 135 140
 Asp Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly
 145 150 155 160
 Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg
 165 170 175
 Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu
 180 185 190
 Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val
 195 200 205
 Lys Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Ala Arg
 210 215 220
 Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln
 225 230 235 240
 Met Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser
 245 250 255
 Ala Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly
 260 265 270
 Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val
 275 280 285
 Phe Pro Leu Leu Met Gly Arg Lys Met Val Ala Gly Ser Gly Ile Gly
 290 295 300
 Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Lys His Asn
 305 310 315 320
 Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
 325 330

<211> 326

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry alcohol dehydrogenase

<400> 31

Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
1 5 10 15

Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
20 25 30

Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
35 40 45

Gly Cys Lys Val Lys Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
50 55 60

Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu
65 70 75 80

Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr
85 90 95

Asp Gly Thr Met Thr Tyr Gly Tyr Ser Asn Asn Met Val Thr Asp
100 105 110

Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala
115 120 125

Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr
130 135 140

Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg
145 150 155 160

Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser
165 170 175

Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Gly Ser Tyr
180 185 190

Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp
195 200 205

Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val
210 215 220

Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn
225 230 235 240

Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro
245 250 255

Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile

260	265	270
Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His		
275	280	285
Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr		
290	295	300
Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile		
305	310	315
Asp Val Glu Asn Thr Leu		
325		
<210> 32		
<211> 278		
<212> PRT		
<213> Fragaria x ananassa		
<220>		
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<400> 32		
Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys Leu		
1	5	10
15		
Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu Asn		
20	25	30
Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp Gly		
35	40	45
Thr Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp Glu Ala		
50	55	60
Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala Pro		
65	70	75
80		
Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe Gly		
85	90	95
Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly Leu		
100	105	110
Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val Thr		
115	120	125
Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His Leu		
130	135	140
Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln Ala		
145	150	155
160		
Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val His		
165	170	175
Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu Val		

180	185	190
Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser Leu		
195	200	205
Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile Lys		
210	215	220
Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr Ala		
225	230	235
Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu Arg		
245	250	255
Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly Asn		
260	265	270
Thr Leu Lys Pro Ala Ile		
275		
<210> 33		
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<220>		
<223> Strawberry alcohol dehydrogenase		
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Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg		
1	5	10
15		
Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile		
20	25	30
Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr		
35	40	45
Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val		
50	55	60
Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly		
65	70	75
80		
Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu		
85	90	95
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr		
100	105	110
Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp		
115	120	125
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala		
130	135	140
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr		
145	150	155
160		

Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly
165 170 175

Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys
180 185 190

Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Ala Leu Lys
195 200 205

His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met
210 215 220

Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala
225 230 235 240

Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys
245 250 255

Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe
260 265 270

Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp
275 280

<210> 34

<211> 188

<212> PRT

<213> Fragaria x ananassa

<220>

<223> Strawberry alcohol dehydrogenase

<400> 34

Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val
1 5 10 15

Val Gly Leu Gly Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala
20 25 30

Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp
35 40 45

Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp
50 55 60

Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp
65 70 75 80

Thr Val Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys
85 90 95

Ala Asn Gly Lys Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu
100 105 110

Leu Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser
115 120 125

Asn Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala
130 135 140

Lys His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu
145 150 155 160

Asn Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe
165 170 175

Val Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr
180 185

<210> 35

<211> 1227

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(979)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 35

g gaa aca gga gca acg gac gta aga ttc aaa gtg ttg tac tgt gga gta 49
Glu Thr Gly Ala Thr Asp Val Arg Phe Lys Val Leu Tyr Cys Gly Val
1 5 10 15

tgc cat tcg gac ata cac atg gcc aaa aat gat tgg ggg act tct acc 97
Cys His Ser Asp Ile His Met Ala Lys Asn Asp Trp Gly Thr Ser Thr
20 25 30

tat cct att gta cct ggg cat gaa ctt gtt ggt gta gta aca gaa gta 145
Tyr Pro Ile Val Pro Gly His Glu Leu Val Gly Val Val Thr Glu Val
35 40 45

gga tgc aaa gta aag aaa ttc aaa agt tgg aga caa ggt cgg tgt tgg 193
Gly Cys Lys Val Lys Phe Lys Ser Trp Arg Gln Gly Arg Cys Trp
50 55 60

ttg cat ggt cga ctc aga cca act tgc gaa aat tgt atc cat cac cta 241
Leu His Gly Arg Leu Arg Pro Thr Cys Glu Asn Cys Ile His His Leu
65 70 75 80

gaa aat tac tgt ccg aat ctg ata caa acc tac ggt tct aaa tac tac 289
Glu Asn Tyr Cys Pro Asn Leu Ile Gln Thr Tyr Gly Ser Lys Tyr Tyr
85 90 95

gac gga acc atg aca tac gga ggt tac tcg aac aac atg gtg act gat 337
Asp Gly Thr Met Thr Tyr Gly Tyr Ser Asn Asn Met Val Thr Asp
100 105 110

gag cac ttc att gtt ccg atc ccg gac aac tta cct ctt gat ggc gct 385
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala

115	120	125	
gct ccg ctt cta tgt gcc ggg att aca act tac agc cca tgg aga tat Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Trp Arg Tyr 130	135	140	433
tat gga ctt gac aaa ccc ggt atg cat ctt ggt gtt gaa tgg cct agg Tyr Gly Leu Asp Lys Pro Gly Met His Leu Gly Val Glu Trp Pro Arg 145	150	155	481
cggtttagg tca cgt ccg tta aat ttg cca ggg ctt tgg ggc tca Arg Phe Arg Ser Arg Pro Pro Leu Asn Leu Pro Gly Leu Trp Gly Ser 165	170	175	529
agg tta cag tca tta gta cct ccc cta att aaa gaa gga ggc agc tat Arg Leu Gln Ser Leu Val Pro Pro Leu Ile Lys Glu Gly Ser Tyr 180	185	190	577
gga aca tct ccc gcg ctg atg cat tcc ctg ctt aga act gac caa gat Gly Thr Ser Pro Ala Leu Met His Ser Leu Leu Arg Thr Asp Gln Asp 195	200	205	625
cag atg gag gct gcc atg agc aca atg gat ggt atc att gac aca gtt Gln Met Glu Ala Ala Met Ser Thr Met Asp Gly Ile Ile Asp Thr Val 210	215	220	673
cct gca gtt cga cct cta gag cct ttg att tca ttg ttg aag act aat Pro Ala Val Arg Pro Leu Glu Pro Leu Ile Ser Leu Leu Lys Thr Asn 225	230	235	721
gga aaa gtt gtt acc gtt ggt ata gca gtg cag cca ctc gat ctc cca Gly Lys Val Val Thr Val Gly Ile Ala Val Gln Pro Leu Asp Leu Pro 245	250	255	769
gtt ttc cct ttg ata ata gga agg aag atg gta gct ggt agt gcc att Val Phe Pro Leu Ile Ile Gly Arg Lys Met Val Ala Gly Ser Ala Ile 260	265	270	817
gga ggt atg aaa gag acg caa gag atg att gat ttt gct gct gaa cat Gly Gly Met Lys Glu Thr Gln Glu Met Ile Asp Phe Ala Ala Glu His 275	280	285	865
aac ata aca gct gac atc gag gtc atc ccg att gat tac ctg aac acc Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr Leu Asn Thr 290	295	300	913
gca atg gaa cgc gtt gtc aaa aaa gat gtc agg ttt cga ttt gtc atc Ala Met Glu Arg Val Val Lys Lys Asp Val Arg Phe Arg Phe Val Ile 305	310	315	961
gac gtt gag aac aca ttg taagtccgcc taagtttttc attcaattct Asp Val Glu Asn Thr Leu 325			1009
gttaataaga ctatgcatta atatatgact gactctccat aggatggagt tatcagtctt caaatttcta gacatatttt gtgatcaaat aaatggaatg gctttgtttt cctttccac			1069
			1129

taagattaga tttcagttgt attgtttta aagagattga tgttttatt aattgtaca 1189
 gtgttacag tctaattcatt aaaaaaaaaa aaaaaaaaaa 1227
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 <213> Fragaria x ananassa
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 <222> (3)..(836)
 <223> partial cDNA
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 <223> Strawberry alcohol dehydrogenase
 <400> 36
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 Lys Val Gln Lys Phe Lys Val Gly Asp Lys Val Gly Val Gly Cys
 1 5 10 15
 ttg gta ggc tca tgc aaa act tgc gac agc tgc gct aac gat ttg gag 95
 Leu Val Gly Ser Cys Lys Thr Cys Asp Ser Cys Ala Asn Asp Leu Glu
 20 25 30
 aac tac tgc ccc aaa cag ata cag act tac ggc gcc aag tac ctt gac 143
 Asn Tyr Cys Pro Lys Gln Ile Gln Thr Tyr Gly Ala Lys Tyr Leu Asp
 35 40 45
 gga aca acc aca tac ggc ggt tac tct gac atc atg gtg ggc gat gag 191
 Gly Thr Thr Tyr Gly Tyr Ser Asp Ile Met Val Ala Asp Glu
 50 55 60
 gcc ttt gta atc cgt att ccg gac aac ctg cct ctt gag ggt gct gct 239
 Ala Phe Val Ile Arg Ile Pro Asp Asn Leu Pro Leu Glu Gly Ala Ala
 65 70 75
 cct ctc cta tgt gcc gga atc aca act tac agt ccc ctg agg tat ttc 287
 Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr Phe
 80 85 90 95
 gga ctt gac aaa ccc ggc atg cat gtc ggg gtg gtt ggc ctt ggc ggt 335
 Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly Gly
 100 105 110
 tta ggc cat gtc gcg gtg aag ttt gcc aag gct ttg ggg gtt aat gtc 383
 Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Leu Gly Val Asn Val
 115 120 125
 aca gtg atc agt acc tcc gct aat aag aaa gat gaa gct att aaa cac 431
 Thr Val Ile Ser Thr Ser Ala Asn Lys Lys Asp Glu Ala Ile Lys His
 130 135 140
 ctt ggt gct gat tct ttc ttg gtc agt cgt gac caa gat cag atg cag 479
 Leu Gly Ala Asp Ser Phe Leu Val Ser Arg Asp Gln Asp Gln Met Gln

145	150	155	
gct gcc atg gga aca ttg gac ggt atc atc gac aca gtt tcc gca gtc			527
Ala Ala Met Gly Thr Leu Asp Gly Ile Ile Asp Thr Val Ser Ala Val			
160	165	170	175
cac ccc ctc cca cct ttg att agt tta ttg aag gct aat gga aag ctt			575
His Pro Leu Pro Pro Leu Ile Ser Leu Leu Lys Ala Asn Gly Lys Leu			
180	185	190	
gtt atg gtt gga gca cca gag aag cca ctt gag cta cca gtt ttt tct			623
Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe Ser			
195	200	205	
tta ata atg gga agg aag act tta gcc ggt agt aat atc gga ggt atc			671
Leu Ile Met Gly Arg Lys Thr Leu Ala Gly Ser Asn Ile Gly Gly Ile			
210	215	220	
aag gag aca caa gag atg ata gat ttg gca gcc aaa cac aac ata acg			719
Lys Glu Thr Gln Glu Met Ile Asp Leu Ala Ala Lys His Asn Ile Thr			
225	230	235	
gcc gac atc gag att atc ccc atc gac tat ttg aac act gct atg gag			767
Ala Asp Ile Glu Ile Ile Pro Ile Asp Tyr Leu Asn Thr Ala Met Glu			
240	245	250	255
cgt ctt gct aaa ggg gat gtt aga tac cgt ttt gtc atc gac atc gga			815
Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg Phe Val Ile Asp Ile Gly			
260	265	270	
aac aca ttg aag ccg gcc att taaatttgca tttcgatcag aaactgaatc			866
Asn Thr Leu Lys Pro Ala Ile			
275			
aagcgaggc gagaggcccta cgtaacaatg caaacatgtg ctagttgtt cttggatgt			926
tcttttagctt ttctctgatg tattccatct gttttgttca tgtcccacatct tattatgaga			986
aaaatgtggg taccgtggat attgaataaa tgaagagcta ctggAACGAT ggTTcacaa			1046
aaaaaaaaaaaa aaaaaaaaaa			1063
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<400> 37			
gca aga gat tca tct ggt gtc ctc tct ccc ttc aat ttc tcc aga agg			48

Ala Arg Asp Ser Ser Gly Val Leu Ser Pro Phe Asn Phe Ser Arg Arg				
1	5	10	15	
gaa acc gga gag aaa gac gtt atg ttc aaa gtg ttg tac tgt gga att				96
Glu Thr Gly Glu Lys Asp Val Met Phe Lys Val Leu Tyr Cys Gly Ile				
20	25	30		
tgc cat tcg gac ctt cac atg gtc aag aat gaa tgg ggc ttc tct acc				144
Cys His Ser Asp Leu His Met Val Lys Asn Glu Trp Gly Phe Ser Thr				
35	40	45		
tat cct ttg gtc ccg ggg cat gag att gtt ggt gaa gtt acg gaa gta				192
Tyr Pro Leu Val Pro Gly His Glu Ile Val Gly Glu Val Thr Glu Val				
50	55	60		
ggg agc aaa gta caa aaa ttt aaa gtt gga gac aga gtc ggt gtt gga				240
Gly Ser Lys Val Gln Lys Phe Lys Val Gly Asp Arg Val Gly Val Gly				
65	70	75	80	
tgc gtt gtg gga tct tgc cga tct tgt gaa aat tgt acc gac cac ctt				288
Cys Val Val Gly Ser Cys Arg Ser Cys Glu Asn Cys Thr Asp His Leu				
85	90	95		
gag aac tac tgc ccc aaa cag ata ctc act tac ggt gcc aag tac tac				336
Glu Asn Tyr Cys Pro Lys Gln Ile Leu Thr Tyr Gly Ala Lys Tyr Tyr				
100	105	110		
gac gga acc acc acc tat ggc ggt tac tct gac att atg gtg gcc gac				384
Asp Gly Thr Thr Tyr Gly Gly Tyr Ser Asp Ile Met Val Ala Asp				
115	120	125		
gaa cac ttc ata gta cgc atc cca gac aac ttg cct ctt gat ggc gct				432
Glu His Phe Ile Val Arg Ile Pro Asp Asn Leu Pro Leu Asp Gly Ala				
130	135	140		
gcg ccg ctc cta tgt gcc ggg att aca acc tac agc ccc ctg aga tat				480
Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr Ser Pro Leu Arg Tyr				
145	150	155	160	
ttc gga ctt gac aag ccc ggc atg cat gta ggt gtg gtc ggc cta ggc				528
Phe Gly Leu Asp Lys Pro Gly Met His Val Gly Val Val Gly Leu Gly				
165	170	175		
ggt tta ggc cac gtc gcc gtg aag ttt gcc aag gct atg gga gtg aag				576
Gly Leu Gly His Val Ala Val Lys Phe Ala Lys Ala Met Gly Val Lys				
180	185	190		
gtt aca gtg atc agt acg tcc cct aag aaa gag gag gaa gct ctt aaa				624
Val Thr Val Ile Ser Thr Ser Pro Lys Lys Glu Glu Ala Leu Lys				
195	200	205		
cac cta gga gct gac tcg ttt ttc gtt agc cgt gac caa gat caa atg				672
His Leu Gly Ala Asp Ser Phe Phe Val Ser Arg Asp Gln Asp Gln Met				
210	215	220		
cag gct gcc att ggt acc atg gat ggg atc att gac aca gtt tct gca				720
Gln Ala Ala Ile Gly Thr Met Asp Gly Ile Ile Asp Thr Val Ser Ala				

225	230	235	240	
caa cat cct ctc ctg cct ttg att ggt ttg ttg aag tct cat gga aag				768
Gln His Pro Leu Leu Pro Leu Ile Gly Leu Leu Lys Ser His Gly Lys				
245.	250	255		
ctt gtt atg gtt ggt gca cca gag aag cct ctt gaa ctt cca gtt ttt	816			
Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu Glu Leu Pro Val Phe				
260	265	270		
cct tta ctc atg gga aga aag atg ggt agc tgg taaccggcat ttgggggtat	869			
Pro Leu Leu Met Gly Arg Lys Met Gly Ser Trp				
275	280			
gaaggagaca caagagatga tagatttgc tgccaggcac aacataacag cagacatcga	929			
agtcatacaa tcgactactt aaacactgct atggagcggt tagtcaaagc agatgtcaga	989			
taccgttttgc tcatcgacat tggaaacaca ctgaaggcta gcacttaat tctgcaatcc	1049			
agactgtatc aatgaagaaa caagaacaga aactgagatt gatttgggtgt catactccgc	1109			
ctatggttt cttacagca tttttgtt tttgctacat gaataacgat cacatgaact	1169			
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gt ccc ctg agg tat ttc gga ctt gac aaa ccc ggc atg cat gtc ggg	47			
Pro Leu Arg Tyr Phe Gly Leu Asp Lys Pro Gly Met His Val Gly				
1	5	10	15	
gtg gtt ggc ctt ggc ggt tta ggc cat gtc gcg gtg aag ttt gcc aag	95			
Val Val Gly Leu Gly Leu Gly His Val Ala Val Lys Phe Ala Lys				
20	25	30		
gct ttg ggg gtt gag gtc aca gtg atc agt acc tcc gct aat aag aaa	143			
Ala Leu Gly Val Glu Val Thr Val Ile Ser Thr Ser Ala Asn Lys Lys				
35	40	45		
gat gaa gct att aaa cac ctt ggt gct gat tct ttc ttg gtc agt cgt	191			
Asp Glu Ala Ile Lys His Leu Gly Ala Asp Ser Phe Leu Val Ser Arg				
50	55	60		
gac caa gat cag cag gct gcc atg gga aca ttg gac ggt atc atc	239			
Asp Gln Asp Gln Met Gln Ala Ala Met Gly Thr Leu Asp Gly Ile Ile				

65	70	75		
gac aca gtt tct gca gtc cac ccc ctc cca cct ttg att agt tta ttg			287	
Asp	Thr	Val	Ser Ala Val His Pro Leu Pro Pro Leu Ile Ser Leu Leu	
80		85	90	95
aag gct aat gga aag ctt gtt atg gtt gga gca cca gag aag cca ctt				335
Lys Ala Asn Gly	Lys	Leu Val Met Val Gly Ala Pro Glu Lys Pro Leu		
100		105	110	
gag cta cca gtt ttt tct tta ata atg gga agg aag act tta gcc ggt			383	
Glu	Leu	Pro Val Phe Ser Leu Ile Met Gly Arg Lys Thr Leu Ala Gly		
115		120	125	
agt aat atc gga ggt atc aag gag aca caa gag atg ata gat ttg gca			431	
Ser	Asn	Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Ile Asp Leu Ala		
130		135	140	
gct aaa cac aac ata acg gcc gac atc gag gtc atc ccc atc gat tat			479	
Ala	Lys	His Asn Ile Thr Ala Asp Ile Glu Val Ile Pro Ile Asp Tyr		
145		150	155	
ttg aac act gca atg gag cgt ctt gct aaa ggg gat gtt aga tac cgg			527	
Leu	Asn	Thr Ala Met Glu Arg Leu Ala Lys Gly Asp Val Arg Tyr Arg		
160		165	170	175
ttt gtc atc gac atc gga aac aca ttg aag ccg gcc act taaatttgc			576	
Phe	Val	Ile Asp Ile Gly Asn Thr Leu Lys Pro Ala Thr		
180		185		
tttcgatcag aaactgaatc aagcgatgtc gagaggccta cgtaacaatg taaacatgt			636	
ctagcttgtt cttgtatgtat ttcttagcat ttctctgatg tactccttct gttttgttca			696	
tgttccatct tataataaga ttcttattat gaaaaaaaaa tggtaccgtg gatattgaat			756	
aaatgaagaa ctactggaac aatggtttca caaattatggtggtgctaa aaaaaaaaaa			816	
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaa aaaaaaa			852	
<210> 39				
<211> 181				
<212> PRT				
<213> Fragaria x ananassa				
<220>				
<223> Strawberry alcohol dehydrogenase				
<400> 39				
Phe Gly Leu Asp Val Gly Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly				
1	5	10	15	
Gly Val Gly His Met Gly Val Lys Ile Ala Lys Ala Met Gly His His				
20	25	30		
Ile Thr Val Ile Ser Ser Asp Lys Lys Lys Lys Glu Ala Leu Glu				
35	40	45		

His Ile Gly Ala Asp Glu Tyr Leu Val Ser Ser Asp Ala Thr Gln Met
 50 55 60

Gln Glu Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Ile Pro Val
 65 70 75 80

Phe His Pro Leu Glu Pro Tyr Leu Ser Leu Leu Lys Leu Asp Gly Lys
 85 90 95

Leu Ile Leu Met Gly Val Ile Asn Thr Pro Leu Gln Phe Val Ser Pro
 100 105 110

Leu Val Met Leu Gly Glu Asp Asp His Arg Glu Leu Cys Gly Glu
 115 120 125

His Glu Gly Asp Gly Gly Asp Ala Arg Val Leu Gln Arg Glu Arg Ala
 130 135 140

Glu Thr Met Ile Glu Val Val Lys Met Asp Tyr Ile Asn Glu Ala Phe
 145 150 155 160

Glu Arg Leu Glu Lys Asn Asp Val Arg Tyr Arg Phe Val Val Asp Cys
 165 170 175

Cys Arg Gln Gln Ser
 180

<210> 40
 <211> 176
 <212> PRT
 <213> Fragaria x ananassa

<220>
 <223> Strawberry alcohol dehydrogenase

<400> 40
 Val His Cys Tyr Ala Tyr Glu Gly Lys Met Gln Glu His Leu Gln Leu
 1 5 10 15

Cys Glu Asp Glu Phe Lys Lys Ile Met Lys Ile Asn Phe Met Ser Ala
 20 25 30

Trp Phe Leu Val Asn Ala Val Gly Arg Arg Met Arg Asp His Lys Ser
 35 40 45

Gly Gly Ser Ile Ile Leu Leu Thr Ser Ile Val Gly Ala Glu Arg Gly
 50 55 60

Leu Tyr Thr Gly Ala Val Ala Tyr Gly Ala Cys Ser Ala Ala Leu Gln
 65 70 75 80

Gln Leu Val Arg Ser Ser Ala Leu Glu Ile Gly Lys Tyr Gln Ile Arg
 85 90 95

Val Asn Ala Ile Ala Arg Gly Leu His Leu Glu Asp Glu Phe Pro Lys
 100 105 110

Ser Val Gly Ile Glu Arg Ala Lys Lys Leu Val Asn Asp Ala Val Pro
 115 120 125
 Leu Glu Arg Trp Leu Asp Val Lys Asn Asp Val Ala Ser Ser Val Ile
 130 135 140
 Tyr Leu Val Ser Asp Gly Ser Arg Tyr Met Thr Gly Thr Thr Ile Phe
 145 150 155 160
 Val Asp Gly Ala Gln Ser Leu Val Arg Pro Arg Met Arg Ser Tyr Met
 165 170 175
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 <400> 41
 Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
 1 5 10 15
 Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
 20 25 30
 Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
 35 40 45
 Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
 50 55 60
 Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
 65 70 75 80
 Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
 85 90 95
 Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
 100 105 110
 Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
 115 120 125
 Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
 130 135 140
 Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
 145 150 155 160
 Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
 165 170 175
 Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
 180 185 190

Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
195 200 205

Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
210 215 220

Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
225 230 235 240

Asp Leu Asn Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val
245 250 255

Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
260 265 270

Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
275 280

<210> 42

<211> 1010

<212> DNA

<213> Fragaria x ananassa

<220>

<221> CDS

<222> (2)..(850)

<223> partial cDNA

<220>

<223> Strawberry alcohol dehydrogenase

<400> 42

g gaa act acc atc aat ttt ggg tct aag aag att gca gtt gtt act gga 49
Glu Thr Thr Ile Asn Phe Gly Ser Lys Lys Ile Ala Val Val Thr Gly
1 5 10 15

gcc aac aaa ggg att gga ctt gag att agc aag caa tta gct gct aaa 97
Ala Asn Lys Gly Ile Gly Leu Glu Ile Ser Lys Gln Leu Ala Ala Lys
20 25 30

gga gtt ggg gtg gta tta aca gca aga gat gtg aag aga gga aca gaa 145
Gly Val Gly Val Val Leu Thr Ala Arg Asp Val Lys Arg Gly Thr Glu
35 40 45

gct gct gaa aat ctt aag gct tct ggg ttc tct gat gtg gta ttt cat 193
Ala Ala Glu Asn Leu Lys Ala Ser Gly Phe Ser Asp Val Val Phe His
50 55 60

cag cta gat gta aca gag ccg act act att ggt tct ttg gca aac ttt 241
Gln Leu Asp Val Thr Glu Pro Thr Thr Ile Gly Ser Leu Ala Asn Phe
65 70 75 80

ctt gaa acg caa ttt gga aag ctt gac ata ttg gtt aac aat gca gga 289
Leu Glu Thr Gln Phe Gly Lys Leu Asp Ile Leu Val Asn Asn Ala Gly
85 90 95

gtc gtt gga tct gta tac ctc aca gcc gac tat gat cca gtg caa aca 337
Val Val Gly Ser Val Tyr Leu Thr Ala Asp Tyr Asp Pro Val Gln Thr
100 105 110

tac gag aca gcg agg gat tgt ttg aaa aca aac tat tat ggg ctc aag 385
 Tyr Glu Thr Ala Arg Asp Cys Leu Lys Thr Asn Tyr Tyr Gly Leu Lys
 115 120 125

caa gtc aca gaa gca ctt gtt ccg ctg ctt caa aaa tct gaa gct gca 433
 Gln Val Thr Glu Ala Leu Val Pro Leu Leu Gln Lys Ser Glu Ala Ala
 130 135 140

agg ata gtc aat gtc tct tcc gga tta gga cag cta aga aat att gga 481
 Arg Ile Val Asn Val Ser Ser Gly Leu Gly Gln Leu Arg Asn Ile Gly
 145 150 155 160

aat gag aag gcc aag aag gag cta gga gat gca gat aac ctc aac gag 529
 Asn Glu Lys Ala Lys Lys Glu Leu Gly Asp Ala Asp Asn Leu Asn Glu
 165 170 175

gag aaa gtg gac aag cta gtt gag gaa ttt ctg gag gat gtg aaa cag 577
 Glu Lys Val Asp Lys Leu Val Glu Glu Phe Leu Glu Asp Val Lys Gln
 180 185 190

gat tcg ata gaa tcc aaa ggc tgg cct cta agt ata tct gcc tac att 625
 Asp Ser Ile Glu Ser Lys Gly Trp Pro Leu Ser Ile Ser Ala Tyr Ile
 195 200 205

gtc tca aaa gca gct ctg aat gct tat aca aga ctc ttg gca aag aag 673
 Val Ser Lys Ala Ala Leu Asn Ala Tyr Thr Arg Leu Leu Ala Lys Lys
 210 215 220

tat ccc cat att gcc ata aac gca gtt ggt cca ggt tat acc aaa aca 721
 Tyr Pro His Ile Ala Ile Asn Ala Val Gly Pro Gly Tyr Thr Lys Thr
 225 230 235 240

gac ctc aat aat aat tcc ggg att ctc aca gtt gaa gaa gct gca gta 769
 Asp Leu Asn Asn Ser Gly Ile Leu Thr Val Glu Glu Ala Ala Val
 245 250 255

ggt cct gtg agg ctg gct ttg ata gcc gaa act aga att tcc ggc ctc 817
 Gly Pro Val Arg Leu Ala Leu Ile Ala Glu Thr Arg Ile Ser Gly Leu
 260 265 270

ttc ttc aac aga aat gaa gag tcg acc ttt gat taggtcaacg tgatccctga 870
 Phe Phe Asn Arg Asn Glu Glu Ser Thr Phe Asp
 275 280

tgaactggac tatttagat tttcagaatg tgcttgattt tgttgaagta tttatggat 930

ttgtatgtat actttgatgt atcattgtat taatagagca catgttgtga tcaaaaaaaaa 990

aaaaaaaaaa aaaaaaaaaa 1010

<210> 43
 <211> 243
 <212> PRT
 <213> Mangifera indica

<220>

<223> Mango esterase

<400> 43

Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser
1 5 10 15

Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
20 25 30

Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Tyr Asn Thr Arg Trp
35 40 45

Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
50 55 60

Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
65 70 75 80

Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
85 90 95

Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
100 105 110

Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
115 120 125

Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
130 135 140

Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
145 150 155 160

Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
165 170 175

Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
180 185 190

Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu
195 200 205

Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
210 215 220

Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
225 230 235 240

Ala Glu Phe

<210> 44

<211> 877

<212> DNA

<213> Mangifera indica

<220>

<221> CDS

<222> (1)..(729)

<223> cDNA

<220>

<223> Mango esterase

<400> 44

atg agg cca caa ata gtg tta ttc gga gat tca ata acg gag caa tct 48
Met Arg Pro Gln Ile Val Leu Phe Gly Asp Ser Ile Thr Glu Gln Ser
1 5 10 15

ttc gga tca ggt ggt tgg ggt tct tct ctt gct gac act tac tct cgc 96
Phe Gly Ser Gly Gly Trp Gly Ser Ser Leu Ala Asp Thr Tyr Ser Arg
20 25 30

aag gct gat gta tta gtt cgt ggc tat ggt ggc tac aat act aga tgg 144
Lys Ala Asp Val Leu Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp
35 40 45

gca ttg ttc ttg tta tgt cac att ttc cct ctg cac aat aaa ata cct 192
Ala Leu Phe Leu Leu Cys His Ile Phe Pro Leu His Asn Lys Ile Pro
50 55 60

cca gcc gtc acc aca att ttc ttt ggg gct aat gat gca gcc ctt ctt 240
Pro Ala Val Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Leu
65 70 75 80

ggg aga acg agt gaa agg cag cat gtt ccc gtg gaa gaa tac aag aac 288
Gly Arg Thr Ser Glu Arg Gln His Val Pro Val Glu Glu Tyr Lys Asn
85 90 95

aat ctc aga aaa atg gtt cag cat ttg aag gaa gtc tcc ccc acg atg 336
Asn Leu Arg Lys Met Val Gln His Leu Lys Glu Val Ser Pro Thr Met
100 105 110

cta gtt gtg ctt att act cca cca cca att gat gag gaa ggg cgt aaa 384
Leu Val Val Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu Gly Arg Lys
115 120 125

gca tat gca cga tcc gtt tat ggt gag aaa gct atg aaa gag cct gag 432
Ala Tyr Ala Arg Ser Val Tyr Gly Glu Lys Ala Met Lys Glu Pro Glu
130 135 140

agg aca aat gaa atg gct gga gtt tat gct aga cat tgt gtt gaa ctg 480
Arg Thr Asn Glu Met Ala Gly Val Tyr Ala Arg His Cys Val Glu Leu
145 150 155 160

gca aaa gat ctt cct gcc att gat ctg tgg tcc aag atg cag gaa aca 528
Ala Lys Asp Leu Pro Ala Ile Asp Leu Trp Ser Lys Met Gln Glu Thr
165 170 175

gaa ggt tgg cag aaa aaa ttc ctc agt gat ggg ttg cac ctt aag tca 576
Glu Gly Trp Gln Lys Lys Phe Leu Ser Asp Gly Leu His Leu Lys Ser
180 185 190

gaa ggc aat gca gtg gtt cac caa gaa gtt gtg aga gtt cta aaa gaa 624
Glu Gly Asn Ala Val Val His Gln Glu Val Val Arg Val Leu Lys Glu

195	200	205	
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gca tgg ttt tct cct gaa caa atg cca tat gat ttt cct cac caa tca 672
 Ala Trp Phe Ser Pro Glu Gln Met Pro Tyr Asp Phe Pro His Gln Ser
 210 215 220

gta att gat gga aaa cac cct gag aaa gct ttc caa ctg caa tgc cct 720
 Val Ile Asp Gly Lys His Pro Glu Lys Ala Phe Gln Leu Gln Cys Pro
 225 230 235 240

gct gaa ttc tagtcaagac aggcttgaa atttgttctc tctttcaatt 769
 Ala Glu Phe

tttctatgg atgaaaagat ttggactgct ttttcctagt catgccaaat gaaacagtgt 829
 tagccttttg cctatggat cagatgctga tatgcgctct gtgtcgac 877

<210> 45
 <211> 12
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: various fruit

<220>
 <223> alcohol acyl transferase motif

<400> 45
 Trp Thr Asn Phe Phe Asn Pro Leu Asp Phe Gly Trp
 1 5 10

<210> 46
 <211> 10
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: various fruit

<220>
 <223> alcohol acyl transferase motif

<220>
 <221> misc_feature
 <222> (1)..(10)
 <223> Xaa is any amino acid residue

<400> 46
 Leu Xaa Xaa Xaa Tyr Pro Xaa Xaa Gly Arg
 1 5 10

<210> 47
 <211> 16
 <212> PRT
 <213> Unknown Organism

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<220>
<223> Description of Unknown Organism: various fruit

<220>
<223> alcohol acyl transferase motif

<220>
<221> misc_feature
<222> (1)..(16)
<223> Xaa is any amino acid residue

<400> 47
Pro Ser Arg Val Xaa Xaa Val Thr Xaa Phe Leu Xaa Lys Xaa Leu Ile
1 5 10 15

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<220>
<221> misc_feature
<222>(9)..(9)
<223> N is Inosine

<400> 48
ggwtgggnk ctaytcttgc 20

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<220>
<223> AAP165

<400> 49
cggatccgga gaaaatttgag gtcag 25

<210> 50
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<220>
<223> AAP166

<400> 50

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cgtcgaccat tgcacgagcc acataatc

28